

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 30, 2000, 14:52:32 ; Search time 40.56 Seconds
(without alignments)
4.088 Million cell updates/sec

Title: US-08-833-506c-120

Perfect score:
33 1 QGILERV 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 188963 seqs, 23686106 residues

Total number of hits satisfying chosen parameters: 76368

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match %

Listing first 100 summaries

Database : A_Geneseq_36:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	100.0	9	1 wB1272	Human iNOS peptide
2	33	100.0	9	1 wB1273	Human iNOS peptide
3	33	100.0	12	1 wB1238	Human iNOS peptide
4	33	100.0	12	1 wB1301	Human iNOS peptide
5	33	100.0	14	1 wB1237	Human iNOS peptide
6	33	100.0	14	1 wB1300	Human iNOS peptide
7	33	100.0	15	1 wB1233	Human iNOS peptide
8	33	100.0	15	1 wB1296	Human iNOS peptide
9	29	87.9	8	1 wB1274	Human iNOS peptide
10	24	72.7	9	1 wB1239	Human iNOS peptide
11	24	72.7	9	1 wB1302	Human iNOS peptide
12	23	69.7	9	1 P93522	Amino acid sequence
13	23	69.7	10	1 R33352	Sequence of trypti
14	23	69.7	15	1 W59122	Peptide K9 express
15	22	66.7	12	1 W81234	Human iNOS peptide
16	22	66.7	12	1 W81297	Human iNOS peptide
17	21	63.6	8	1 P93513	Amino acid sequenc
18	21	63.6	9	1 R49676	Human leucocyte an
19	21	63.6	13	1 P93520	Amino acid sequenc
20	21	63.6	15	1 W59086	FMDV non-structura
21	20	60.6	5	1 R62202	CENP-B protein ami
22	20	60.6	7	1 W66560	Peptide useful as
23	20	60.6	8	1 R73346	Human TSH receptor
24	20	60.6	8	1 R73347	Human TSH receptor
25	20	60.6	11	1 R77218	Mouse anti-human I
26	20	60.6	14	1 R65049	Random biotinylati
27	20	60.6	14	1 W11550	FGF9 antigenic pep
28	20	60.6	14	1 W46652	Biotinylation pept
29	20	60.6	15	1 P90253	Antigenic Peptide
30	19	57.6	4	1 W46528	Peptide containing
31	19	57.6	11	1 W87171	Peptide determined
32	19	57.6	7	1 R1398	VPI peptide used t
33	19	57.6	7	1 W38293	Poxvirus amino a
34	19	57.6	8	1 P51212	Analgesic Peptide.

ALIGNMENTS

RESULT
W81272

ID W81272 standard; peptide; 9 AA.
 AC W81272;
 DT 30-APR-1999 (first entry)
 DE Human iNOS Peptide fragment PS-5275.
 CC Inducible nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 myocardial infarction; tissue rejection; transplantation; psoriasis;
 autoimmune disease; multiple sclerosis.
 OS Homo sapiens.
 Key
 FH Modified_site 9 /note= "Val residue amidated"
 FT Location/Qualifiers
 PN W09845710-A1.
 PD 15-OCT-1998.
 PF 11-APR-1997; U06500.
 PR 07-APR-1997; US-677777.
 PA (WEBB/) WEBBER R.
 PI Webber R.
 DR 98:594:95/50
 PT Detection of human inducible nitric oxide synthase - using an
 immunoassay in which a sample is contacted with a specific binding
 entity reactive with human iNOS or mimics.
 PS Example 13: Page 55; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 specific binding entity (e.g. a monoclonal antibody) reactive to human
 inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 to detect the presence of human iNOS protein in the sample. The method
 can be used for the detection and quantitation of human iNOS in cells and
 tissues for various pathophysiological conditions such as sepsis, septic
 shock, myocardial infarction, rejection of tissue in organs following
 transplantation, monitoring "flare ups" in certain autoimmune diseases
 such as lupus, psoriasis, and multiple sclerosis. This sequence
 represents a peptide from human iNOS which is used in the method of the
 invention.
 CC Sequence 9 AA;

Query Match 100.0%; Score 33; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Key
 FH Modified_site 9 /note= "Val residue amidated"
 FT Location/Qualifiers
 PN W09845710-A1.
 PD 15-OCT-1998.
 PF 11-APR-1997; U06500.
 PR 07-APR-1997; US-677777.
 PA (WEBB/) WEBBER R.
 PI Webber R.
 DR 98:594:95/50.
 PT Detection of human inducible nitric oxide synthase - using an
 immunoassay in which a sample is contacted with a specific binding
 entity reactive with human iNOS or mimics.
 PS Example 4; Page 37; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 specific binding entity (e.g. a monoclonal antibody) reactive to human
 inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 to detect the presence of human iNOS protein in the sample. The method
 can be used for the detection and quantitation of human iNOS in cells and
 tissues for various pathophysiological conditions such as sepsis, septic
 shock, myocardial infarction, rejection of tissue in organs following
 transplantation, monitoring "flare ups" in certain autoimmune diseases
 such as lupus, psoriasis, and multiple sclerosis. This sequence
 represents a peptide from human iNOS which is used in the method of the
 invention.
 CC Sequence 12 AA;

Query Match 100.0%; Score 33; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.38;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Key
 FH Modified_site 9 /note= "Val residue amidated"
 FT Location/Qualifiers
 PN W09845710-A1.
 PD 15-OCT-1998.
 PF 11-APR-1997; U06500.
 PR 07-APR-1997; US-677777.
 PA (WEBB/) WEBBER R.
 PI Webber R.
 DR 98:594:95/50.
 PT Detection of human inducible nitric oxide synthase - using an
 immunoassay in which a sample is contacted with a specific binding
 entity reactive with human iNOS or mimics.
 PS Example 13: Page 55; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 specific binding entity (e.g. a monoclonal antibody) reactive to human
 inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 to detect the presence of human iNOS protein in the sample. The method
 can be used for the detection and quantitation of human iNOS in cells and
 tissues for various pathophysiological conditions such as sepsis, septic
 shock, myocardial infarction, rejection of tissue in organs following
 transplantation, monitoring "flare ups" in certain autoimmune diseases
 such as lupus, psoriasis, and multiple sclerosis. This sequence
 represents a peptide from human iNOS which is used in the method of the
 invention.

DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment for epitope mapping #22.
DE Inducible nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis; epitope mapping.
OS Homo sapiens.
PN WO944510-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI; 98-594495/50.
PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Fig 7C; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention.
SQ Sequence 12 AA:

Query Match 100.0%; Score 33; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 0.38;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILERV 7
ID W81237 standard; peptide; 14 AA.
AC W81237;
DB 5 QGILERV 11

RESULT 5
W81237
ID W81237 standard; peptide; 14 AA.
AC W81237;
DT 30-APR-1999 (first entry)
DE Human iNOS Peptide fragment PS-5226.
KW Inducible nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key
FT Location/Qualifiers
FT Modified_site 14
FT /note= "Gly residue amidated"
PN WO944510-A1.
PD 15-OCT-1998.
PF 11-APR-1997; U06500.
PR 07-APR-1997; US-667777.
PA (WEBB/) WEBBER R.
PI Webber R.
DR WPI; 98-594495/50.

PT Detection of human inducible nitric oxide synthase - using an
PT immunoassay in which a sample is contacted with a specific binding
PT entity reactive with human iNOS or mimics.
PS Example 4; Page 37; 93pp; English.
CC This invention describes an immunoassay method where a sample with a
CC specific binding entity (e.g. a monoclonal antibody) reactive to human
CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
CC to detect the presence of human iNOS protein in the sample. The method
CC can be used for the detection and quantitation of human iNOS in cells and
CC tissues for various pathophysiological conditions such as sepsis, septic
CC shock, myocardial infarction, rejection of tissue in organs following
CC transplantation, monitoring "flare ups" in certain autoimmune diseases
CC such as lupus, psoriasis, and multiple sclerosis. This sequence
CC represents a peptide from human iNOS which is used in the method of the
CC invention.
SQ Sequence 14 AA:

Query Match 100.0%; Score 33; DB 1; Length 14;

Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGILERV 7
ID W81233 standard; peptide; 15 AA.
AC W81233;
DB 5 QGILERV 11

RESULT 7
W81233
ID W81233 standard; peptide; 15 AA.
AC W81233;
DT 30-APR-1999 (first entry)
DE Human iNOS peptide fragment PS-5222.
KW Inducible nitric oxide synthase; iNOS; human; immunoassay; detection;
KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
KW myocardial infarction; tissue rejection; transplantation; psoriasis;
KW autoimmune disease; multiple sclerosis.
OS Homo sapiens.
FH Key
FT Location/Qualifiers

Location/Qualifiers

PR 07-APR-1997; US-667777.
 PA (WEBB) WEBBER R.
 PT Webber R;
 DR WPI; 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 entity reactive with human iNOS or mimics.
 PT immunoassay in which a sample is contacted with a specific binding
 entity reactive with human iNOS or mimics.
 PS Example 4; Page 47; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 specific binding entity (e.g. a monoclonal antibody) reactive to human
 inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 to detect the presence of human iNOS protein in the sample. The method
 can be used for the detection and quantitation of human iNOS in cells and
 tissues for various pathophysiological conditions such as sepsis, septic
 shock, myocardial infarction, rejection of tissue in organs following
 transplantation, monitoring "flare ups" in certain autoimmune diseases
 such as lupus, psoriasis, and multiple sclerosis. This sequence
 represents a peptide from human iNOS which is used in the method of the
 invention. Sequence 9 AA;

Query Match 72.7%; Score 24; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGILE 5
 Db 5 QGILE 9

RESULT 11
 ID W81302 standard; Peptide; 9 AA.
 AC W81302 standard; Peptide; 9 AA.
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment for epitope mapping #23.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 myocardial infarction; tissue rejection; transplantation; psoriasis;
 autoimmune disease; multiple sclerosis; epitope mapping.
 OS Homo sapiens.
 PN W09845710-A1.
 PD 15-OCT-1998.
 PR 11-APR-1997; U06500.
 PA (WEBB) WEBBER R.
 PT Webber R;
 DR WPI; 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 entity reactive with human iNOS or mimics.
 PS Example 4; Fig 7C; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 specific binding entity (e.g. a monoclonal antibody) reactive to human
 inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 to detect the presence of human iNOS protein in the sample. The method
 can be used for the detection and quantitation of human iNOS in cells and
 tissues for various pathophysiological conditions such as sepsis, septic
 shock, myocardial infarction, rejection of tissue in organs following
 transplantation, monitoring "flare ups" in certain autoimmune diseases
 such as lupus, psoriasis, and multiple sclerosis. This sequence
 represents a peptide from human iNOS which is used in the method of the
 invention. Sequence 9 AA;

Query Match 72.7%; Score 24; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGILE 5

Db 5 QGILE 9

RESULT 12
 ID P93522 standard; protein; 9 AA.
 AC P93522;
 DT 03-JUN-1990 (first entry)
 DE Amino acid sequence of polylinker region of transfer vector pBF129
 KW Polyhedrin protein; silkworm nuclear polyhedrosis virus; NPV;
 HIV gene; gag; pol; SOR; gp120; gp41; polylinker region.
 PN J01071990-A.
 PD 20-MAR-1989.
 PR 17-SEP-1987; 231107.
 DR WPI; 89-127530/17.
 PT New transfer vector pBFs, for HIV diagnosis
 PT contg. promoter region of polyhedrin protein gene for silk-worm
 PT nuclear polyhedrosis virus deoxyribonucleic acid
 PT Figure 2; Page 9; 11pp; Japanese.
 CC Transfer vectors pBFs were prep'd. contg. promoter region of polyhedrin
 protein gene of silkworm nuclear polyhedrosis virus (NPV) recombinant
 CC with HIV gene gag, pol, SOR, gp120 or gp41 in the polylinker region
 CC of the vector. Thus, HIV antigenic protein can be produced in large
 CC amounts and used as an antigen for the diagnosis of HIV or for
 CC vaccine production.
 SQ Sequence 9 AA;

Query Match 69.7%; Score 23; DB 1; Length 9;
 Best Local Similarity 66.7%; Pred. No. 1.5e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGILER 6
 :||||:
 Db 3 EGILDR 8

RESULT 13
 ID R33352 standard; Peptide; 10 AA.
 AC R33352;
 DT 30-JUN-1993 (first entry)
 DE Sequence of tryptic peptide derived form purine-rich repeat (GA
 DE repeat) binding protein (GABP) at peptide 1.
 KW GA binding protein; GABP; cis-regulatory element; VP16 mediated induction.
 OS Synthetic.
 PN W09304166-A.
 PD 04-MAR-1993.
 PR 006748.
 PA (CARN-) CARNegie INST WASHINGTON.
 PT Lamarcro KL, Mc Knight SL, Thompson CC;
 DR WPI; 93-09398/11.
 PT DNA encoding GA binding protein sub-unit - allows investigation
 PT of sub-unit sequence motif functions, for control of rapid cell
 division e.g. in cancer.
 PS Disclosure; Page 3; 68pp; English.
 CC A cis-regulatory element required for virion associated protein VP16
 CC mediated induction of herpes simplex virus 1 (HSV) immediate early
 CC (IE) genes consists of three imperfect repeats of the purine-rich
 CC hexanucleotide 5'-CGGAA-3'. A protein complex capable of avid
 CC interaction with the purine-rich repeats (GA repeats) has been
 CC identified in soluble preparations of rat liver nucleic. This GA
 CC binding protein (GABP) consists of two separable subunits.
 CC Applicants have isolated cDNA clones encoding both subunits of GABP
 CC and have revealed that one (GABP alpha) is related to the Ets
 CC transforming protein, while the other (GABP beta) contains a
 CC series of 33-amino acid repeats related in sequence to a variety
 CC of proteins.

CC represents a peptide from human iNOS which is used in the method of the
CC invention.
SC Sequence 12 AA;

Query Match	66.7%	Score 22;	DB 1;	Length 12;
Best Local Similarity	100.0%	Pred. No.	83;	
Matches	5;	Mismatches	0;	Indels 0;
Qy	3 ILERV 7	Gaps 0;		
Db	1 ILERV 5			

RESULT 17

P93513	standard; protein: 8 AA.
ID	P93513;
AC	
DT	03-JUN-1990 (first entry)
DE	Amino acid sequence of polylinker region of transfer vector pBFS5
KW	Polyhedrin protein; silkworm nuclear polyhedrosis virus; NPV;
KW	HIV gene gag; pol; SOR; gp120; gp41; polylinker region; pBFS5.
PN	J017490-A.
PD	20-MAR-1989.
PF	17-SEP-1987; 231107.
PR	17-SEP-1987; JP-231107.
PA	(MAED) Maeda S.
PI	WPI: 89-127530/17.
DR	N-PSDB: N92289.
PT	New transfer vector PBFS, for HIV diagnosis -
PT	contg. promoter region of polyhedrin protein gene for silk-worm
PT	nuclear polyhedrosis virus deoxyribonucleic acid
PS	Figure 2; page 9; 11pp; Japanese.
CC	Transfer vectors PBFS were prep. contg. promoter region of polyhedrin
CC	nuclear polyhedrosis virus (NPV) recombinant protein gene of silkworm nuclear polyhedrosis virus (NPV) recombined
CC	with HIV gene gag, pol, SOR, gp120 or gp41 in the polylinker region
CC	of the vector. Thus, HIV antigenic protein can be produced in large
CC	amounts, and used as an antigen for the diagnosis of HIV or for
CC	vaccine production.
SQ	Sequence 8 AA;

CC an HLA-DQ4 molecule. The peptide is used for the treatment of autoimmune disease, especially for treatment of allergies.

Query Match	63.6%	Score 21;	DB 1;	Length 9;
Best Local Similarity	80.0%	Pred. No.	1.5e+05;	
Matches	4;	Mismatches	1;	Indels 0;
Qy	2 GILER 6	Gaps 0;		
Db	3 GILDR 7			

RESULT 19

P93520	standard; protein: 13 AA.
ID	P93520;
AC	P93520;
DT	03-JUN-1990 (first entry)
DE	Amino acid sequence of polylinker region of transfer vector pBFS1
KW	Polyhedrin protein; silkworm nuclear polyhedrosis virus; NPV;
KW	HIV gene gag; pol; SOR; gp120; gp41; polylinker region; pBFS1.
PN	J010490-A.
PD	20-MAR-1989.
PF	17-SEP-1987; 231107.
PR	17-SEP-1987; JP-231107.
PA	(MAED) Maeda S.
PI	WPI: 89-127530/17.
DR	N-PSDB: N92396.
PT	New transfer vector PBFS, for HIV diagnosis -
PT	contg. promoter region of polyhedrin protein gene for silk-worm
PT	nuclear polyhedrosis virus deoxyribonucleic acid
PS	Figure 2; page 9; 11pp; Japanese.
CC	Transfer vectors PBFS were prep. contg. promoter region of polyhedrin
CC	protein gene of silkworm nuclear polyhedrosis virus (NPV) recombinant protein gene of silkworm nuclear polyhedrosis virus (NPV) recombined
CC	with HIV gene gag, pol, SOR, gp120 or gp41 in the polylinker region
CC	of the vector. Thus, HIV antigenic protein can be produced in large
CC	amounts, and used as an antigen for the diagnosis of HIV or for
CC	vaccine production.
SQ	Sequence 13 AA;

Query Match	63.6%	Score 21;	DB 1;	Length 13;
Best Local Similarity	80.0%	Pred. No.	1.5e+02;	
Matches	4;	Mismatches	1;	Indels 0;
Qy	2 GILER 6	Gaps 0;		
Db	3 GILDR 7			

RESULT 20

W90086	standard; peptide: 15 AA.
ID	W90086
AC	W90086;
DT	10-AUG-1998 (first entry)
DE	FMDV non-structural viral protein immunogenic Peptide fragment #14. Foot and Mouth disease; FMDV; immunogenic; viral nonstructural protein; SyntheCic.
KW	Bos taurus.
OS	DE19638044-A1.
PN	DE19638044-A1.
PD	19-MAR-1998.
PF	18-SEP-1996; 038044.
PR	18-SEP-1996; DE-138044.
PA	(FARB) BAYER AG
PI	Correa R, Froehlich B, Glatthaar-Saalmueller B, Hehnen H,
PI	Pauli T, Pfaffe E, Saalmueller A, Wiesmueller K,
DR	WIT: 98-180328/17.
PT	Vaccines against foot and mouth disease virus - comprising peptide fragments of nonstructural viral proteins
CC	Claim 1; Page 14; 27pp; German.
CC	W59073-W59119 are immunogenic peptides from a foot and mouth disease

CC virus (FMDV) nonstructural protein which are immunoreactive with CC FMDV-specific antibodies or T cells and can be used in vaccines against the disease. The vaccines are used especially for immunising CC pigs and cattle.
Sequence 15 AA;

Query Match 63.6%; Score 21; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.7e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 2 GILBER 6
Db 9 GILEK 13

RESULT 21
ID R62202 standard; Protein; 5 AA.
AC R62202
DT 03-MAY-1995 (first entry)
DE CENP-B protein amino acids 473-477, homologous to HSV-1 IE motif.
KW CENP-B protein; centromere protein; epitope;
KW autoantibody; immunoinfective cluster virus; nuclear protein antigen;
KW systemic rheumatic disorder; herpes simplex virus; HSV-1 IE;
KW immediate early protein; systemic lupus erythematosus; scleroderma.
OS Homo sapiens.
PN W0942011-A.
PD 15-SEP-1994.
PR 10-MAR-1993; US-02631.
PA (UWSC-) UNIV SOUTHERN CALIFORNIA.

Douvas A, Ehresmann G, Takehana Y;
WPI: 94-302659/37.
DR R73346 standard; Peptide; 8 AA.
PT Methods for treating immunoinfective cluster virus infections -
PT utilise antibodies or fragments characteristic of auto antibodies
PT produced by patients with rheumatic disorders
PS Disclosure; Page 73; 106pp; English.
CC A comparison of the CENP-B centromere protein sequence with proteins
CC from immunoinfective cluster viruses revealed widespread
CC homologies. The importance of these homologous motifs is that they
CC are epitopes for autoantibodies occurring in high titres in systemic
CC rheumatic disorders. Seras from such patients could be used for
CC treatment of immunoinfective cluster virus infections, e.g. HIV-1,
CC immunoinfective adenoviruses, human lymphotropic retroviruses,
CC rubella virus, CMV and EBV infections.
Sequence 5 AA;

Query Match 60.6%; Score 20; DB 1; Length 5;
Best Local Similarity 60.0%; Pred. No. 1.5e+05; Indels 0; Gaps 0;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGILE 5
Db 1 QGIVE 5

RESULT 22
ID W66560 standard; Peptide; 7 AA.
AC W66560
DT 26-NOV-1998 (first entry)
DE peptide useful as angiogenesis inhibitor.
KW anti-angiogenic drug; cancer; arthritis; retinopathy; angiogenesis;
KW inhibitor; cancer; arthritis; eye disease; macular degeneration;
KW retinopathy.
OS Synthetic.
FH Location/Qualifiers
FT Modified_site 1 /note= "Optional N-terminal acetyl"
FT Misc_difference 3 /note= "D-form residue"

CC virus (FMDV) nonstructural protein which are immunoreactive with CC FMDV-specific antibodies or T cells and can be used in vaccines CC against the disease. The vaccines are used especially for immunising CC pigs and cattle.
Sequence 15 AA;

/note= "Optionally Arg-NH2 or Arg-NHCH2CH3"

FT Modified_site 7 /note= "Optionally Arg-NH2 or Arg-NHCH2CH3"
FT FT
PN WO84152-A1.
PD 24-SEP-1998.
PF 16-MAR-1998; US-05327.
PR 17-MAR-1997; US-120667.

PA (ABBO) ABBOTT LAB.
PA (NODIN) UNIV NORTHWESTERN.
PA DR
WPI: 98-521165/44.
PT New peptide(s) containing D-amino acid residues as angiogenesis inhibitors - for example, for cancer, arthritis, eye diseases
PT New peptides relating to peptides of formulae (I)-(IV): T-Gly-Val-D-Ile-Thr-Arg-Ile-U (I), V-Gly-D-Val-Ile-W (II), X-D-Arg-D-Ile-W (III), X-D-Arg-D-Ile-D-Arg-D-Thr-Ile-D-Val-Y (IV).
The invention relates to peptides of formulae (I)-(IV): T-Gly-Val-D-Ile-Thr-Arg-Ile-U (I), V-Gly-D-Val-Ile-W (II), X-D-Arg-D-Ile-U (IV).
T is absent or is an N-protecting group or 1-12 amino acids, optionally terminated by an N-protecting group; U = Arg or Arg-NR1R2; R1 and R2 = hydrogen and 1-4C alkyl; V and X are absent or N-protecting groups
W = D-Arg or D-Arg-NR1R2; Y = Gly or Gly-NR1R2; Z = 1-12 amino acids, optionally terminated by a protecting group and including at least one D-amino acid. The peptides are inhibitors of angiogenesis (they inhibit migration of endothelial cells) and are useful for treatment of cancer, arthritis, psoriasis, infections of, or surgical injury to, the eye, macular degeneration or diabetic retinopathy. They can also be used for treating other autoimmune or ocular diseases, blood vessel disease, example of an angiogenesis inhibitor disclosed in the specification.
Sequence 7 AA;

Query Match 60.6%; Score 20; DB 1; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.5e+05;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
SQ Sequence 7 AA;

RESULT 23
ID R73346 standard; Peptide; 8 AA.
AC R73346
DB 1 GILBER 7
Qy 1 :::::
Db 1 GVIKRI 6

RESULT 23
ID R73346 standard; Peptide; 8 AA.
AC R73346
DT 12-DEC-1995 (first entry)
DE Human TSH receptor (residues 291-298).
KW thyroid stimulating hormone receptor; TSH; human; Homo sapiens;
KW antibody; affinity; detection.
OS Synthetic.
PN J07089991-A.
PD 04-APR-1995.
PR 28-SEP-1993; 240853.
PR 28-SEP-1993; JP-240853.
PA (MITSUBISHI PETROCHEMICAL CO LTD.
DR WPI: 95-167251/22.
PT Novel polypeptide(s) having affinity for the human TSH receptor antibody - used in detection of the TSH antibody.
PS Example 1; Page 25; 54pp; Japanese.
CC Peptides with affinity to human TSH (thyroid stimulating hormone)
CC receptor antibody are used for detection of the antibody. (See also R73201-592).
SQ Sequence 8 AA;

Query Match 60.6%; Score 20; DB 1; Length 8;
Best Local Similarity 80.0%; Pred. No. 1.5e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
SQ Sequence 8 AA;

Query Match 60.6%; Score 20; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.5e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QGIE 5
Db 3 RGILE 7

RESULT 24		Query Match	Match	Score 20;	DB 1;	Length 11;
ID	Best Local Similarity	Pred.	No. 2e+02;	Mismatches	Indels	Gaps
AC	Matches 5;	Conservative	0;	0;	0;	0;
R73347	standard; Peptide: 8 AA.	Qy	1 QGILERV 7			
R73347;		Db				
DT	12-DEC-1995 (first entry)		3 QGILVTV 9			
DE	Human TSH receptor (residues 293-300).					
KW	thyroid stimulating hormone receptor; TSH; human; Homo sapiens;					
KW	antibody; affinity; detection.					
OS	Synthetic.					
PN	J07089991-A.	RESULT 26				
PD	04-APR-1995.	ID	R65049 standard; Peptide: 14 AA.			
PF	28-SEP-1993; 240853.	AC	R65049;			
PR	28-SEP-1993; JP-240853.	DT	24-OCT-1995 (first entry)			
(MTP)	MITSUBISHI PETROCHEMICAL CO LTD.	DE	Random biotinylation peptide 17.			
DR	WPI: 95-167251/22.	KW	biotinylation; peptide; recombinant; fusion protein; small;			
PT	Novel polypeptide(s) having affinity for the human TSH receptor antibody - used in detection of the TSH antibody.	KW	specific; defined; purification; BirA; enzyme; biotin.			
PS	Example 1; Page 25; 54pp; Japanese.	OS	Synthetic.			
CC	Peptides with affinity to human TSH receptor antibody are used for detection of the antibody. (See also R73201-52).	Key				
CC		modified_site 9				
SQ	Sequence 8 AA;	FT	/note= "Biotin-Lys"			
		FT	WO504069-A.			
		PN	09-FEB-1995.			
		PD	09-FEB-1995.			
		PF	28-JUL-1994; U08528.			
		PR	30-JUL-1993; US-059991			
		(AFFYX) AFFYMAX TECHNOLOGIES NV.				
		PI	Schatz, RJ;			
		DR	WP1; 95-090609/12.			
		PT	Production of biotinylated proteins by expression of a recombinant DNA vector - which encodes a fusion protein comprising a protein and a biotinylated peptide.			
		PT	Claim 10; Page 136; 14pp; English.			
		CC	A library of small, efficient peptide biotinylation sequences (W65048-66)			
		CC	was generated by using a generic peptide (R65047) and a system known as the "peptides on plasmids" system. At some positions in the sequences, no clear consensus is apparent. At other residues, however, clear trends emerge. A protein can be biotinylated by constructing a recombinant DNA expression vector encoding a fusion protein, comprising a protein and a biotinylation peptide. A host cell, e.g. E. coli, is transformed with the vector and is cultured in the presence of biotin and a biotinylation enzyme, e.g. BirA.			
		PS	Sequence 14 AA;			
		SQ				
Query Match		Score 20;	DB 1;	Length 8;		
Best Local Similarity	Pred.	No. 1.5e+05;				
Matches	4;	Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 QGILE 5					
Db	1 RGILE 5					
Query Match		Score 20;	DB 1;	Length 8;		
Best Local Similarity	Pred.	No. 1.5e+05;				
Matches	4;	Conservative	1;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1 QGILE 5					
Db	1 RGILE 5					
Query Match		Score 20;	DB 1;	Length 14;		
Best Local Similarity	Pred.	No. 2.6e+02;				
Matches	4;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1 QGILE 5					
Db	2 QGIFB 6					
Query Match		Score 20;	DB 1;	Length 14;		
Best Local Similarity	Pred.	No. 2.6e+02;				
Matches	4;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1 QGILE 5					
Db	2 QGIFB 6					
Query Match		Score 20;	DB 1;	Length 14;		
Best Local Similarity	Pred.	No. 2.6e+02;				
Matches	4;	Conservative	0;	Mismatches 1;	Indels 0;	Gaps 0;
Qy	1 QGILE 5					
Db	2 QGIFB 6					
RESULT 27						
ID	W11550 standard; Peptide: 14 AA.					
AC	W11550					
DT	19-SEP-1997 (first entry)					
CC	FGR9 antigenic peptide, SP32.					
CC	Mouse; chicken; fibroblast growth factor 9; FGFR9; detection;					
CC	fibroblast growth factor receptor 3; FGFR3; cartilage repair;					
CC	bone repair; antagonist; anti-FGR9 antibody; endochondromas;					
CC	solitary hereditary exostosis; multiple hereditary exostosis;					
CC	KW halux valgus deformity; achondroplasia; synovial chondromatosis.					
OS	Synthetic.					
PN	W0641523-A.					
PD	27-DEC-1994.					
PF	30-MAY-1994; J00859.					
PA	31-MAY-1994; JP-129787.					
PA	(CHUS) CHUGAI SEIYAKU KK.					
PA	(CHUS) CHUGAI PHARM CO LTD.					
PI	Hirata, Y., Sato, K., Tsuchiya, M.					
DR	WPI: 95-022828/03.					
PT	Antibody against IL-6 - useful for the therapy and treatment of IL-6 related disorders.					
PS	Claim 13; Page 66; 82pp; Japanese.					
CC	The sequence of the mouse anti-human interleukin-6 (IL-6) antibody heavy chain variable region framework region (FR) 4. The sequences of FR1-4 (R77215-8) were used in conjunction with the complementarity determining regions 1-3 (R77212-4) to construct a chimaeric antibody against human interleukin-6 (IL-6). The vectors Q5914-7 express constructs encoding fragments of a chimaeric antibody to the human IL-6 comprising (a) a light chain with (i) a variable region containing 3 CDR (R77201-3) inserted into several framework regions (FR) (R77204-7) and (ii) a human light chain constant region and (b) a heavy chain with (i) a variable region containing 3 CDR (R7721-4) inserted into FR (R7715-8) and (ii) a human light chain constant region. The FR of the light chain may be mouse derived (Q75888) or from the human antibody RET. The heavy chain FR may also be mouse derived (Q75888) or from the human antibody DSW. The antibodies can be used in the treatment of IL-6 related disorders. The antibodies are useful as they have low antigenicity due to the use of human derived sequences and low antigenicity mouse derived sequences.					
CC	Sequence 11 AA;					

PT recombinant fibroblast growth factor 9 DNA
 Example 1; Page 7; 32pp; English.
 CC The sequences given in WI1549-50 represent antigenic peptide fragments
 CC of fibroblast growth factor 9 (FGF9) which were used in the production
 CC of anti-FGF9 antibodies. FGF9 is used in the method of the invention
 CC for detecting fibroblast growth factor receptor 3 (FGFR3) in a sample
 CC or tissue. The method comprises contacting the sample or tissue with
 CC FGF9, allowing formation of receptor-ligand pairs, and detecting any
 CC FGF9-FGF9 pairs. Compositions containing FGF9 can be used to increase
 CC FGF3 activity, esp. to stimulate cartilage or bone repair. Compositions
 CC containing FGF9 antagonists or FGF9 binding agents (e.g. anti-FGF9
 CC antibodies) can be used to treat diseases caused by an excess of FGF9
 CC or overactivity of FGFR3, esp. multiple or solitary hereditary exostosis,
 CC hallux valgus deformity, achondroplasia, synovial chondromatosis and
 CC endochondromas. Sequence 14 AA;

Query Match 60.6%; Score 20; DB 1; Length 14;
 Best Local Similarity 66.7%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 QGILER 6
 :||| |
 Db 4 KGILRR 9

RESULT 28
 W46652 standard; peptide; 14 AA.
 AC W46652;
 DT 28-MAY-1998 (first entry)
 DE Biotinylation peptide isolated from random library 2.
 KW Biotinylation Peptide; biotinylation enzyme; biotin-protein ligase;
 KW BirA; biotin ligase; biotin; purification; immobilisation; labelling;
 KW Synthetic.
 OS US5723584 A.
 PN PD 03-MAR-1998.
 PF 03-FEB-1995; 383753.
 PR 30-JUL-1993; US-099991.
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 PI Schatz PJ.
 WPI: 98-178542/16.
 DR Peptide(s) that can be biotylated by biotin ligase - and fusion
 PT proteins containing them
 Claim 3: Column 66; 33pp; English.

Peptides W46651-69 are non-naturally occurring biotinylation peptides,
 CC derived from a library constructed to express peptides of the generic
 sequence W46650. The library was constructed using oligonucleotides
 CC W1621-22. The peptides contain a biotinylatable sequence motif,
 CC recognised by a biotinylation enzyme, e.g. biotin-protein ligase (BirA).
 The C or N terminus of the peptides can be covalently coupled to a
 CC protein that is incapable of being biotinylated by a biotin ligase.
 The peptides can be biotinylated in vitro or in vivo, especially with
 CC BirA biotin ligase, and used for the purification, immobilisation,
 CC labelling or detection of proteins. Sequence 14 AA;

Query Match 60.6%; Score 20; DB 1; Length 14;
 Best Local Similarity 80.0%; Pred. No. 2.6e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QGILE 5
 :||| |
 Db 2 QGIFE 6

Query Match 60.6%; Score 20; DB 1; Length 15;
 Best Local Similarity 60.0%; Pred. No. 2.7e+02; Indels 0; Gaps 0;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGILE 5
 :||| |
 Db 1 QGVVE 5

RESULT 30
 ID W46528 standard; peptide; 4 AA.
 AC W46528;
 DT 20-MAY-1998 (first entry)
 DE Peptide containing a protease binding site,
 KW protease binding site; Protease; Protease indicator; fluorescent signal;
 KW detection; protease activity.
 OS Synthetic.
 PN US514342 A.
 PD 03-FEB-1998.
 PF 27-OCT-1995; 549008.
 PR 27-OCT-1995; US-549008.
 PA (ONO-) ONCOMUNIN INC.
 PI Komoriya A; Packard BS;
 DR WPI-15834/14.
 PT Fluorogenic substrates for protease determination - having two
 closely spaced fluorophores flanking protease binding site
 Disclosure; Column 4; 39pp; English.
 PS Peptides W46520-53 contain protease binding sites. They are used to
 CC produce novel reagents whose fluorescence increases in the presence of
 particular proteases. These fluorogenic protease indicators (substrates)
 CC provide a high intensity fluorescent signal at a visible wavelength when
 CC they are digested by a protease. The fluorogenic indicators have the
 general formula:
 CC F1-C1--P--C2--F2
 | |
 (S1)n (S2)k
 where:
 CC P is a peptide containing a protease binding site, e.g. W46520-53.
 CC F1 and F2 are fluorophores.
 CC S1 and S2 are peptide spacers e.g. W46554-58.
 CC n, k = 0 or 1.
 CC C1 and C2 are conformation-determining regions that introduce a bend
 CC into the conformation which positions the fluorophores adjacent to each
 CC other with a separation of less than 100 Angstrom.
 CC when n is 1, S1 is joined to the terminal alpha -amino group of C1 by a
 CC peptide bond, and when k is 1, S2 is joined to the terminal carboxy group

RESULT 29
 P90253 standard; peptide; 15 AA.
 ID P90253
 AC P90253;

CC of C2 by a peptide bond. The protease indicators are used for detecting
CC protease activity in a biological sample. The sample is contacted with
CC the indicator and any change in fluorescence is detected, an increase in
CC fluorescence indicating protease activity.
SQ Sequence 4 AA;

```
Query Match      57.68;  Score 19;  DB 1; Length 4;  
Best Local Similarity 100.0%;  Pred. No. 1.5e-05;  
Matches 4;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;  
Qy  1 QGIL 4  
    |||  
Db  1 QGIL 4
```

Search completed: June 30, 2000, 14:52:36
Job time: 6003 sec

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OM protein - protein search, using sw model

Run on: June 30, 2000, 14:54:15 ; Search time 50.08 Seconds
 (without alignments)
 8.195 Million cell updates/sec

Title: US-08-833-506C-120
 Perfect score: 33
 Sequence: 1 QGILERV 7

Scoring table: BLOSUM62

Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen parameters: 2577

Minimum DB seq length: 0
 Maximum DB seq length: 15

Post-processing: Minimum Match 08
 Listing first 100 summaries

Database : PIR_63;*

1: pir;*

2: pir;*

3: pir;*

4: pir;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	21	63.6	15	2	PA0076	fructose-bisphosphochlorophyll a/b-bi-acetyl-CA carboxy
2	19	57.6	14	2	S50900	T-cell receptor be
3	19	57.6	14	2	S35267	lipid transfer pro
4	18	54.5	9	2	PH0942	Ig heavy chain J r
5	18	54.5	15	2	A53085	hemolytic protein
6	17	51.5	15	2	PS0382	MUC1 enhancer bind
7	16	48.5	13	2	S09018	16K Protein - Pouli
8	16	48.5	14	2	A59018	fructose-bisphosph
9	15	45.5	10	2	S19295	T antigen variant
10	15	45.5	13	2	I58003	Ig heavy chain CRD
11	15	45.5	14	2	S29789	hypothetical prote
12	15	45.5	14	2	S03530	cytochrome-c oxida
13	15	45.5	14	2	S65392	fructose-bisphosph
14	15	45.5	15	2	PA0075	bradykinin-potenti
15	15	45.5	15	2	PA0102	pyridoxal kinase
16	15	45.5	15	2	A61483	(ornithine decarbox
17	14	42.4	7	2	PT0246	outer membrane por
18	14	42.4	10	2	S06964	148K exoantigen -
19	14	42.4	10	2	B56899	T-cell receptor be
20	14	42.4	11	1	XASNBA	T-cell receptor ga
21	14	42.4	11	1	A61483	aminotransferase C
22	14	42.4	11	2	S34065	sperm motility inh
23	14	42.4	12	2	B58503	ribosomal protein
24	14	42.4	12	2	C33099	gene HEXA protein
25	14	42.4	12	2	PH1467	ALL ALIGNMENTS
26	14	42.4	12	2	H41946	
27	14	42.4	12	4	JX0315	
28	14	42.4	13	2	S66235	
29	14	42.4	14	2	S66234	
30	14	42.4	14	2	C44823	

Description

fructose-bisphosphochlorophyll a/b-bi-acetyl-CA carboxy	Ig heavy chain V-D-J r
hypothetical prote	myosin, gizzard -
lipid transfer pro	RNA-binding protei
Ig heavy chain J r	self-incompatibili
hemolytic protein	7.5K surfactant-as
MUC1 enhancer bind	gallbladder stone
16K Protein - Pouli	fructose-2,6-bisph
fructose-bisphosph	collagen type I -
T antigen variant	Ig H chain V-D-J r
Ig heavy chain CRD	pyruvate dehydroge
hypothetical prote	T-cell receptor al
cytochrome-c oxida	hydrogen sulfate re
fructose-bisphosph	acylaminacyl Pept
bradykinin-potenti	beta-neendorphin
pyridoxal kinase	seed storage prote
(ornithine decarbox	ferredoxin--NADP+
outer membrane por	cytchrome P450 (1
148K exoantigen -	carnitine medium/l
T-cell receptor be	kinase activator P
T-cell receptor ga	probable antigen 5
aminotransferase C	ribosomal protein
sperm motility inh	gene HEXA protein
ribosomal protein	ALL ALIGNMENTS

RESULT 1
PA0076 fructose-bisphosphate aldolase (EC 4.1.2.13) - fungus (*Fusarium sporotrichioides*) (fragment)
C;Species: *Fusarium sporotrichioides*
C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995
C;Accession: PA0076
R;Chow, L.P.; Fukay, N.; Sugura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A;Reference number: PA0051
A;Molecule type: protein
A;Residues: 1-15 <CHO>
C;Keywords: aldehyde-lyase; carbon-carbon lyase

Query Match Score 57.6%; Best Local Similarity 28.6%; Pred. No. 3.7e+02; Length 14;
Matches 5; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
PH0942 T-cell receptor beta chain V-D-J region (clone 13) - rat (fragment)
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbergk, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allele
A;Reference number: PH0891; MUID:92078857
A;Accession: PH0942
A;Molecule type: mRNA
A;Residues: 1-9 <GOLD>
A;Experimental source: complete Freund's adjuvant-immunized lymph node
A;Note: the authors translated the codon TGC for residue 2 as Ala
C;Keywords: T-cell receptor

Query Match Score 54.5%; Best Local Similarity 60.0%; Pred. No. 1.3e+02; Length 9;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
A53085 lipid transfer protein - rabbit (fragment)
C;Species: *Oryctolagus cuniculus* (domestic rabbit)
C;Date: 13-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C;Accession: A53085
R;Ko, K.W.; Oikawa, K.; Ohnishi, T.; Kay, C.M.; Yokoyama, S.
Biochemistry 32, 6729-6736, 1993
A;Title: Purification, characterization, and conformational analysis of rabbit plasma
A;Reference number: A53085; MUID:93320050
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <KO1>
A;Experimental source: plasma
A;Note: sequence extracted from NCBI backbone (NCBIP:135263)

Query Match Score 54.5%; Best Local Similarity 50.0%; Pred. No. 6.7e+02; Length 15;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

RESULT 6
PS0382 Ig heavy chain J region 2 - rat (fragment)
C;Species: *Rattus norvegicus* (Norway rat)
C;Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 06-Jun-1997
C;Accession: PS0382
R;Lang, P.; Mocikat, R.
Gene 102, 261-264, 1991
A;Title: Immunoglobulin heavy-chain joining genes in the rat: comparison with mouse and human
A;Reference number: JH0666; MUID:91340162

Query Match Score 57.6%; Best Local Similarity 28.6%; Pred. No. 3.7e+02; Length 14;
Matches 5; Mismatches 0; Indels 0; Gaps 0;

RESULT 2
S50900 chlorophyll a/b-binding protein Lhcbs5 - spinach (fragment)
N;Alternate names: light-harvesting complex LHCIIc protein
C;Species: *Spinacia olaracea* (spinach)
C;Date: 19-Mar-1997 #sequence_revision 23-Apr-1999 #text_change 23-Apr-1999
C;Accession: S50900
R;Walters, R.G.; Ruban, A.V.; Horton, P.
Eur. J. Biochem. 226, 1053-1059, 1994
A;Title: Higher plant light-harvesting complexes LHCIIa and LHCIIc are bound by dicyclohexil
A;Reference number: S50900; MUID:95112835
A;Accession: S50900
A;Molecule type: protein
A;Residues: 1-14 <WAL>
C;Superfamily: chlorophyll a/b-binding protein
C;Keywords: chlorophyll; chloroplast; light-harvesting complex; photosynthesis; photosys-

Query Match Score 57.6%; Best Local Similarity 60.0%; Pred. No. 3.7e+02; Length 14;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Query Match Score 57.6%; Best Local Similarity 28.6%; Pred. No. 3.7e+02; Length 14;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

RESULT 3
S35267 acetyl-CoA carboxylase (EC 6.4.1.2) - wheat (fragment)
C;Species: *Triticum aestivum* (common wheat)
C;Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C;Accession: S35267
R;Gornicki, P.; Haselkorn, R.
Plant Mol. Biol. 22, 547-552, 1993
A;Title: Wheat acetyl-CoA carboxylase
A;Reference number: S35267; MUID:93320392
A;Accession: S35267
A;Molecule type: protein
A;Residues: 1-14 <GOR>
A;Experimental source: leaf
C;Function:
A;Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA
A;Pathway: fatty acid biosynthesis
C;Keywords: fatty acid biosynthesis; ligase

A;Accession: PS0382
A;Molecule type: DNA
A;Residues: 1-15 <LAN>
A;Cross-references: EMBL:X56791
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin

Query Match 51.5%; Score 17; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 3; Conservative 2; Indels 0; Gaps 0;

Qy 1 QGILERV 7
Db 7 QGVNVTY 13

RESULT 7
S09018 hemolytic protein Al - edible frog (fragment)
C;Species: Rana esculenta (edible frog)
C;Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993
C;Accession: S09018
R;Sammaco, M.; De Biase, D.; Severini, C.; Aita, M.; Ersperer, G.F.; Barra, D.; Bossa, F.
Biochim. Biophys. Acta 1033, 318-323, 1990
A;Title: Purification and characterization of bioactive peptides from skin extracts of R
A;Reference number: S09018; MUID:90189865
A;Accession: S09018
A;Molecule type: protein
A;Residues: 1-13 <STM>

Query Match 48.5%; Score 16; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 3; Conservative 2; Indels 0; Gaps 0;

Qy 2 GILERV 7
Db 7 GILSQL 12

RESULT 8
A59018 MUC1 enhancer binding protein 70K chain MUC1EBP-70 - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 08-May-1998
R;Ade, M.; Smith, C.J.; Larson, C.J.
A;Description: Submitted to the Protein Sequence Database, May 1998.
A;Reference number: A59018
A;Accession: A59018
A;Molecule type: protein
A;Residues: 1-14 <ABE>
A;Experimental source: breast cancer cell line MCF-7
A;Note: 3'-val was also found
C;Keywords: DNA binding; heterodimer

Query Match 48.5%; Score 16; DB 2; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Indels 0; Gaps 0;

Qy 1 QGILER 6
Db 9 QIILEK 14

RESULT 9
S19296 16K protein - pouillard wheat
C;Species: Triticum turridum (pouillard wheat)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997

C;Accession: S19296
R;Sanchez-Monge, R.; Gomez, L.; Barber, D.; Lopez-Otin, C.; Armentia, A.; Salcedo, G.
Biochem. J. 281, 401-405, 1992
A;Title: Wheat and barley allergens associated with baker's asthma. Glycosylated subu
A;Reference number: S19296; MUID:92143804
A;Accession: S19296
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-10 <SBN>

Query Match 45.5%; Score 15; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 2; Conservative 2; Indels 0; Gaps 0;

Qy 2 GILE 5
Db 7 GLME 10

RESULT 10
I58003 hprt protein - Chinese hamster (fragment)
C;Species: Cricetus griseus (Chinese hamster)
C;Date: 19-Mar-1997 #sequence_revision 07-Nov-1997 #text_change 14-Nov-1997
C;Accession: I58003
R;Eusco, J.C.; Zimmerman, L.J.; Fekete, A.; Setzer, R.W.; Rossiter, B.J.
Mutat. Res. 269, 171-181, 1992
A;Title: Analysis of X-ray-induced Hprt mutations in CHO cells: insertion and deletio
A;Reference number: I58003; MUID:93024355
A;Accession: I58003
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-13 <RES>
A;Cross-references: GB:S46270; NID:g257049
C;Genetics:
A;Gene: hprt

Query Match 45.5%; Score 15; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Indels 0; Gaps 0;

Qy 4 LERV 7
Db 1 LEKV 4

RESULT 11
S29789 hypothetical protein - thermoplasma acidophilum (fragment)
C;Species: Thermoplasma acidophilum
C;Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C;Accession: S29789
R;Bright, J.R.; Byrom, D.; Danson, M.J.; Hough, D.W.; Tower, P.
Bur. J. Biochem. 211, 549-551, 1993
A;Title: Cloning, sequencing and expression of the gene encoding glucose dehydrogenas
A;Reference number: S29788; MUID:93170285
A;Accession: S29789
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-14 <BRI>
A;Cross-references: EMBL:X59788

Query Match 45.5%; Score 15; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
Matches 2; Conservative 3; Indels 0; Gaps 0;

Qy 3 ILERV 7
Db 4 LLKRI 8

A; Note: this form (I) had a molecular weight of 30.6K and an isoelectric point of 5.3
 RESULT 12
 S03530
 19 heavy chain J region (JH-4) - African clawed frog
 C; Species: Xenopus laevis (African clawed frog)
 C; Date: 21-Nov-1993 #sequence_revision 08-Nov-1996 #text_change 09-Sep-1997
 C; Accession: S03530
 R; Schiwyer, J.; Grossberger, D.; du Pasquier, L.
 EMBL J. 7, 2409-2415, 1988
 A; Title: Organization and rearrangement of immunoglobulin M genes in the amphibian xenopus
 A; Reference number: S01158; MUID:89052653
 A; Accession: S03530
 A; Molecule type: DNA
 A; Residues: 1-14 <SCH>
 A; Cross-references: EMBL:X14916; NID:964805; PID:e16056; PID:91334657

Query Match Score 45.5%; Score 15; DB 2; Length 14;
 Best Local Similarity 57.1%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Gaps 0;
 Indels 0;

Qy 1 QGILERV 7
 Db 6 QGtLVTV 12

RESULT 13
 S65392
 cytochrome-c oxidase (EC 1.9.3.1) chain VIII-L - rat (fragment)
 C; Species: Rattus norvegicus (Norway rat)
 C; Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 07-May-1999
 C; Accession: S65392; S65333; S65391
 R; Schaeffer, H.; Noack, H.; Halangk, W.; Brandt, U.; von Jatow, G.
 Eur. J. Biochem. 230, 235-241, 1995
 A; Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-terminal sequence number: S65372; MUID:95324529
 A; Accession: S65392
 A; Status: preliminary
 A; Molecule type: Protein
 A; Residues: 1-14 <SCH>
 A; Accession: S65393
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 1-14 <SSC2>
 A; Accession: S65391
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 1-14 <SG3>
 C; Keywords: oxidoreductase

Query Match Score 45.5%; Score 15; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 3.1e+03;
 Matches 2; Conservative 2; Gaps 0;
 Indels 0;

Qy 2 GILE 5
 Db 11 GTLD 14

RESULT 14
 PA0075
 fructose-bisphosphate aldolase (EC 4.1.2.13) I - fungus (Fusarium sporotrichioides) (fragment)
 N; Alternate names: aldolase; fructose-1,6,-bisphosphate triosephosphate-lyase
 C; Species: Fusarium sporotrichioides
 C; Accession: PA0075; PA0077
 C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 10-Nov-1995
 R; Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 Submitted to JIPID, October 1994
 A; Reference number: PA0051
 A; Accession: PA0075
 A; Molecule type: protein
 A; Residues: 1-15 <CHO>

A; Note: this form (I) had a molecular weight of 30.6K and an isoelectric point of 5.3
 A; Accession: PA0077
 A; Molecule type: protein
 A; Residues: 1-15 <CH2>
 A; Note: this form (II) had a molecular weight of 31.6K and an isoelectric point of 5.
 C; Keywords: aldehyde-de-lyase; carbon-carbon lyase

Query Match Score 45.5%; Score 15; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 1; Gaps 0;
 Indels 0;

Qy 1 QGILER 6
 Db 3 QEVLSR 8

RESULT 15
 PA0102
 fructose-bisphosphate aldolase (EC 4.1.2.13) III - fungus (Fusarium sporotrichioides)
 C; Species: Fusarium sporotrichioides
 C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-Mar-1995
 C; Accession: PA0102
 C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 03-Mar-1995
 R; Chow, L.P.; Fukaya, N.; Sugiura, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
 submitted to JIPID, October 1994
 A; Reference number: PA0051
 A; Accession: PA0102
 A; Molecule type: protein
 A; Residues: 1-15 <CHO>

Query Match Score 45.5%; Score 15; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 1; Gaps 0;
 Indels 0;

Qy 1 QGILER 6
 Db 3 QEVLSR 8

RESULT 16
 PH1377
 T antigen variant K-5 - mouse (fragment)
 C; Species: Mus musculus (house mouse)
 C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C; Accession: PH1377
 R; Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.
 J. Exp. Med. 176, 449-457, 1992
 A; Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for
 A; Reference number: PH1373
 A; Accession: PH1377
 A; Status: preliminary
 A; Molecule type: mRNA
 A; Residues: 1-15 <LIID>

Query Match Score 45.5%; Score 15; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 3; Conservative 0; Gaps 0;
 Indels 0;

Qy 1 QGI 3
 Db 1 QGI 3

RESULT 17
 PT0246
 Ig heavy chain CRD3 region (clone 2-103D) - human (fragment)
 C; Species: Homo sapiens (man)
 C; Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C; Accession: PT0246
 R; Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991
 A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j
 A:Reference number: PR0222; MUID:91108337
 A:Accession: PT0446
 A:Molecule type: DNA
 A:Residues: 1-7 <YAM>
 A:Experimental source: B lymphocyte
 C:Keywords: heterotetramer; immunoglobulin

Query Match Score 14; DB 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GIL 4
 Db 5 GIL 7

RESULT 18
 S06964 hypothetical protein (nifa' 5' region) - Rhizobium leguminosarum (fragment)
 C:Species: Rhizobium leguminosarum
 C:Accession: S06964
 C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 08-Oct-1999
 R:Roelvink, P.W.; Hontelez, J.G.J.; van Kammen, A.; van den Bos, R.C.
 Mol. Microbiol. 3, 1431-1447, 1989
 A:Title: Nucleotide sequence of the regulatory nifa gene of Rhizobium leguminosarum PRE:
 A:Reference number: S06964; MUID:90136072
 A:Accession: S06964
 A:Molecule type: DNA
 A:Residues: 1-10 <ROE>
 A:Cross references: ENBL:X17073; NID:946208; PIDN:CAA34923.1; PID:9809748

Query Match Score 14; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 3.8e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 2 GILE 5
 Db 5 GILK 8

RESULT 19
 B56899 serum heterodimer, 24K chain - sandbar shark (fragment)
 C:Species: Carcharhinus plumbeus (sandbar shark)
 C:Accession: B56899
 C:Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 11-Aug-1995
 R:Vazquez-Moreno, L.; Porath, J.; Schluter, S.F.; Marchalonis, J.J.
 Comp. Biochem. Physiol. B Comp. Biochem. 103, 563-568, 1992
 A:Reference number: A56899; MUID:9302592
 A:Accession: B56899
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-10 <VAZ2>
 C:Keywords: glycoprotein; plasma

Query Match Score 14; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 ERV 7
 Db 5 ERV 7

RESULT 20
 XSNBNA bradykinin-potentiating peptide B - mamushi

C:Species: Agkistrodon blomhoffi (mamushi)
 C:Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 08-Dec-1995
 C:Accession: A01254
 R:Kato, H.; Suzuki, T.
 Proc. Jpn. Acad. 46, 176-181, 1970
 A:Reference number: A01254
 A:Accession: A01254
 A:Molecule type: protein
 A:Residues: 1-11 <SKAT>
 A:Note: the sequence of the natural peptide was confirmed by the synthesis and analysis
 C:Superfamily: bradykinin-potentiating peptide
 C:Keywords: angiotensin-converting enzyme inhibitor; bradykinin; pyroglutamic acid; v
 F:1/Modified site: pyrrolidine carboxylic acid (Gln) #status experimental

Query Match Score 14; DB 1; Length 11;
 Best Local Similarity 50.0%; Pred. No. 4.2e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 OGILER 6
 Db 1 QGLPPR 6

RESULT 21
 A1483 pyridoxal kinase (EC 2.7.1.35) - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Accession: A1483
 C:Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994
 R:Churchich, J.E.
 J. Protein Chem. 9, 613-621, 1990
 A:Title: Cleavage of pyridoxal kinase into two structural domains: kinetics of proteo
 A:Reference number: A61483; MUID:91197387
 A:Accession: A61483
 A:Status: preliminary
 A:Molecule type: Protein
 A:Residues: 1-11 <CHU>
 C:Keywords: homodimer; phosphotransferase

Query Match Score 14; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 4.2e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 ILER 6
 Db 8 VLQR 11

RESULT 22
 S34065 ornithine decarboxylase - mouse
 C:Species: Mus musculus (house mouse)
 C:Accession: S34065
 R:Tsirka, S.E.; Turck, C.W.; Coffino, P.
 Biochem. J. 293, 289-295, 1993
 A:Title: Multiple active conformers of mouse ornithine decarboxylase.
 A:Reference number: S34065; MUID:93319524
 A:Accession: S34065
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-11 <TSI>

Query Match Score 14; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 4.2e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LERY 7
 Db 7 LDRI 10

RESULT 23
 B58503 outer membrane porin OprD homolog - unidentified bacterium (fragment)
 N; Alternate names: 43K bille stone protein
 C; Species: unidentified bacterium
 C; Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 10-Jul-1998
 R; Binette, J.-P.; Binette, M.B.
 submitted to the Protein Sequence Database, October 1996
 A; Description: The proteins of kidney and gallbladder stones.
 A; Accession: B58503
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 1-12 <BIN>
 A; Experimental source: human bile with stones
 A; Note: sequenced along with secondary sequence MXIGVYNEXL

Query Match 42.4%; Score 14; DB 2; Length 12;
 Best Local Similarity 40.0%; Pred. No. 4.5e+03; Indels 0; Gaps 0;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QGI 5
 Db 7 KGFIIE 11

RESULT 24
 C33099 14Bk exoantigen - Plasmodium falciparum (fragment)
 C; Species: Plasmodium falciparum
 C; Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 18-Aug-1992
 C; Accession: C33099
 R; Nichols, J.R.; Hager, L.P.
 submitted to the Protein Sequence Database, May 1990
 A; Accession number: A33098
 A; Accession: C33099
 A; Status: preliminary
 A; Molecule type: protein
 A; Residues: 1-12 <NIC>

Query Match 42.4%; Score 14; DB 2; Length 12;
 Best Local Similarity 66.7%; Pred. No. 4.5e+03; Indels 0; Gaps 0;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGI 3
 Db 3 QGV 5

RESULT 25
 PH1467 T-cell receptor beta chain (clone 223/27) - mouse (fragment)
 C; Species: Mus musculus (house mouse)
 C; Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 11-Apr-1995
 R; Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Regnault, A.; Ko J. Exp. Med. 177 811-820, 1993
 A; Title: T cell receptor selection by and recognition of two class I major histocompatibility genes
 A; Reference number: PH1430; MUID:93171821
 A; Molecule type: mRNA
 A; Residues: 1-12 <CAS>
 A; Experimental source: cytolytic T-lymphocyte
 C; Superfamily: Immunoglobulin homology
 C; Keywords: receptor; T-cell

Query Match 42.4%; Score 14; DB 2; Length 12;

Best Local Similarity 66.7%; Pred. No. 4.5e+03; Indels 0; Gaps 0;

Qy 1 QGI 3
 Db 7 QGV 9

RESULT 26
 H41946 T-cell receptor gamma chain (5t.12) - mouse (fragment)
 C; Species: Mus musculus (house mouse)
 C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 07-May-1999
 C; Accession: H41946
 R; Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R. Mol. Cell. Biol. 11, 5902-5909, 1991
 A; Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma A; Reference number: A41946; MUID:92049316
 A; Accession: H41946
 A; Status: preliminary; not compared with conceptual translation
 A; Molecule type: DNA
 A; Residues: 1-12 <WHE>
 C; Keywords: T-cell receptor

Query Match 42.4%; Score 14; DB 2; Length 12;
 Best Local Similarity 67.7%; Pred. No. 4.5e+03; Indels 0; Gaps 0;

Qy 1 QGI 3
 Db 5 QGV 7

RESULT 27
 JX0315 amino transferase chimera DY18 - synthetic (fragment)
 C; Species: synthetic
 C; Date: 28-May-1999 #sequence_revision 28-May-1999 #text_change 28-May-1999
 C; Accession: JX0315
 R; Miyazawa, K.; Kawaguchi, S.; Okamoto, A.; Kato, R.; Ogawa, T.; Kuramitsu, S. J. Biochem. 115, 58-57, 1994
 A; Title: Construction of aminotransferase chimeras and analysis of their substrate specificity
 A; Reference number: JX0315; MUID:94334304
 A; Accession: JX0315
 A; Molecule type: DNA
 A; Residues: 1-12 <MIVY>
 C; Comment: This enzyme is a chimeric enzyme of Escherichia coli aspartate aminotransferase and glutamate synthase. The parent enzymes catalyze the reversible amino group transfer reaction
 C; Keywords: aminotransferase

Query Match 42.4%; Score 14; DB 4; Length 12;
 Best Local Similarity 50.0%; Pred. No. 4.5e+03; Indels 0; Gaps 0;

Qy 1 QGI 3
 Db 5 QGV 7

RESULT 28
 S66235 sperm motility inhibitor protein - pig (fragment)
 C; Species: Sus scrofa domestica (domestic pig)
 C; Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C; Accession: S66235
 R; Iwamoto, T.; Hiroaki, H.; Furuchi, Y.; Wada, K.; Satoh, M.; Osada, T.; FEBS Lett. 368, 420-424, 1995
 A; Title: Cloning of boar SPIN gene which is expressed specifically in seminal vesicle
 A; Reference number: S66233; MUID:95361914
 A; Accession: S66235
 A; Status: preliminary

A;Molecule type: protein
 A;Residues: 1-13 <IWA>
 A;Note: Pro-6 was also found

Query Match 42.4%; Score 14; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 4.9e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 GILE 5
 Db 10 GVLR 13

RESULT 29

S66234
 sperm motility inhibitor protein - pig (fragment)
 C;Species: Sus scrofa domestica (domestic pig)
 C;Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
 C;Accession: S66234
 R;Iwamoto, T.; Hiroaki, H.; Furuchi, Y.; Wada, K.; Satoh, M.; Osada, T.; Gag
 FEBS Lett. 368, 420-424, 1995
 A;Title: Cloning of boar SPMI gene which is expressed specifically in seminal vesicle an
 A;Reference number: S66233; MUID:95361914
 A;Accession: S66234
 A;Status: Preliminary
 A;Molecule type: protein
 A;Residues: 1-14 <IWA>
 A;Note: Phe-9 and Phe-12 were also found

Query Match 42.4%; Score 14; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 5.3e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 GILE 5
 Db 11 GVLR 14

RESULT 30

C44823
 synaptosomal-associated protein SNAP-25 peptide 8 - rabbit (fragment)
 N;Alternate names: synapsin peptide 8
 C;Species: Oryctolagus cuniculus (domestic rabbit)
 C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 15-Jun-1996
 C;Accession: C44823
 R;Loewy, A.; Liu, W.S.; Baitinger, C.; Willard, M.B.
 J. Neurosci. 11, 3412-3421, 1991
 A;Title: The major 35S-methionine-labeled rapidly transported protein (superprotein) is
 A;Reference number: A44823; MUID:9204785
 A;Accession: C44823
 A;Status: Preliminary
 A;Molecule type: protein
 A;Residues: 1-14 <LOE>
 A;Experimental source: visual tissue
 A;Note: sequence extracted from NCBI backbone (NCBIP:64253)
 C;Keywords: membrane trafficking

Query Match 42.4%; Score 14; DB 2; Length 14;
 Best Local Similarity 100.0%; Pred. No. 5.3e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 LER 6
 Db 12 LER 14

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 30, 2000, 19:03:14 ; Search time 39.08 Seconds

(without alignments)
5.455 Million cell updates/sec

Title: US-08-833-506C-120

Gapext 0.5

1 QGILERV 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 83857 seqs, 30454973 residues

Total number of hits satisfying chosen parameters:

668

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : Swissprot_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	20	60.6	15	1	ATP2_PINPS	P81663	pinus pinas
2	16	48.5	13	1	HPL_RANES	P52415	rana escula
3	16	48.5	13	1	NPM_HUMAN	P51910	homo sapien
4	15	45.5	14	1	YGDH_THEAC	Q05213	thermoplasm
5	15	45.5	15	1	CDD2_ITIGI	P56247	litoria gil
6	14	42.4	10	1	TRPB_LEUMA	P81737	leucophaea
7	14	42.4	11	1	BPPB_AGHKA	P01021	agistrodon
8	14	42.4	12	1	CD11_LITXA	P56245	litoria xan
9	14	42.4	12	1	CD14_LITXA	P56246	litoria xan
10	14	42.4	13	1	CHEP_PARID	P42718	parapolybia
11	14	42.4	13	1	FIBB_HYLAL	P14472	hylobates
12	14	42.4	14	1	FIBB_MANLE	P14474	mandrillus
13	14	42.4	14	1	MY14_EISFO	P46979	eisenia foetida
14	14	42.4	14	1	UN37_CLOPA	P81338	clostridium
15	14	42.4	15	1	LPL_THETH	P21234	thermus aqu
16	14	42.4	15	1	MALT_BACTQ	P80072	bacillus th
17	13	39.4	12	1	PA2B_VIPBO	P31859	vipera berus
18	13	39.4	12	1	UP01_GAEEL	P55934	caenorhabdi
19	13	39.4	13	1	CRBL_VESCR	P01518	vespa crabro
20	13	39.4	13	1	FARB_ASCUS	P43173	ascaris suu
21	13	39.4	13	1	HPB9_RANES	P32416	rana escula
22	13	39.4	14	1	CRBL_VESOR	P17236	vespa orientalis
23	13	39.4	14	1	IF2G_RAT	P81795	rattus norvegicus
24	13	39.4	14	1	MY14_PHEVI	P46980	pharotima v
25	12	36.4	6	1	ACP_RABIT	P25514	oryctolagus cuniculus
26	12	36.4	10	1	CU30_LOCM1	P11735	locusta migratoria
27	12	36.4	10	1	TRP9_LEUMA	P81741	leucophaea
28	12	36.4	10	1	URAL_HUMAN	P32118	homo sapien
29	12	36.4	11	1	CH60_DROME	P35380	drosophila
30	12	36.4	13	1	CRBL_JCAPSP	P17237	icaria sp.
31	12	36.4	13	1	CRBL_VESAN	P17233	vespa analis
32	12	36.4	13	1	CRBL_VESMA	P17332	vespa manda
33	12	36.4	13	1	CRBL_VESTR	P17231	vespa tropica
34	12	36.4	13	1			

ALIGNMENTS

RESULT 1
ATP2_PINPS

ID ATP2_PP1NPS STANDARD; PRT; 15 AA.
 AC P81663;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE ATP SYNTHASE BETA CHAIN, MITOCHONDRIAL (EC 3.6.1.34) (FRAGMENT).
 GN ATPB.
 OS Pinus pinaster (Maritime Pine).
 OC Euphyllophytes; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferales; Pinaceae;
 RN [1]
 RP
 SEQUENCE.
 RC TISSUE-NEEDLE;
 RX MEDLINE: 99274088.
 RA Costa F., Pilonneau C., Bauw G., Dubos C., Bahriman N., Kremer A.,
 RA Frigerio J.-M., Flomion C.;
 RT "Separation and characterization of needle and xylem maritime pine
 proteins";
 RT "Proteins".
 RL Electrophoresis 20:1098-1108(1999).
 CC -1- FUNCTION: PRODUCES ATP FROM ADP IN THE PRESENCE OF A PROTON
 GRADIENT ACROSS THE MEMBRANE. THE BETA CHAIN IS THE CATALYTIC
 CC -1- SUBUNIT (BY SIMILARITY).
 CC -1- SUBUNIT: F-TYPE ATPASES HAVE 2 COMPONENTS, CF(1) - THE CATALYTIC
 CORE - AND CF(0) - THE MEMBRANE PROTON CHANNEL, CF(1) HAS FIVE
 CC SUBUNITS: ALPHA (3), BETA (3), GAMMA (1), DELTA (1), EPSILON (1). CF (0)
 CC HAS THREE MAIN SUBUNITS: A, B AND C.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC (SPOT N153) IS: 5.5 , ITS MW IS: 55 KD.
 CC -1- SIMILARITY: BELONGS TO THE ATPASE ALPHA/BETA CHAINS FAMILY.
 DR PS00152; ATPase_alpha_beta; PARTIAL.
 KW ATP synthase; CF(1); Hydrolase; ATP-binding; Mitochondrion.
 KW Hydrolase; ATP-binding; Mitochondrion.
 FT 1
 NON_TER 15
 FT 15 AA; 1629 MW; 35B8CBB725CCB8D9 CRC64;
 SQ

Query Match Score 60.6%; Pred. No. 1.2e+02; Length 15;
 Best Local Similarity 60.0%; Mismatches 2; Indels 0; Gaps 0;

Qy 1 QGILE 5
 Db 7 QVLD 11

RESULT 2
 ID HPA1_RANES STANDARD; PRT; 13 AA.
 AC P32415;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE HEMOLYTIC PROTEIN A1 (FRAGMENT).
 OS Rana esculenta (Edible frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 OC Batrachia; Anura; Neobatrachia; Ranodea; Ranidae; Ranae; Rana.
 RN [1]
 RP
 SEQUENCE.
 RC TISSUE-SKIN SECRETION;
 RX MEDLINE: 90198965.
 RA Slumacco M., de Blas D., Severini C., Alita M., Ersperer G.F.,
 RA Barra D., Bossa F.;
 RT "Purification and characterization of bimacitive peptides from skin
 extracts of Rana esculenta";
 RL Blochim. Biophys. Acta 103:318-323(1990).
 CC -1- FUNCTION: SHOWS HEMOLYTIC ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 DR PIR: S09018; S09018
 KW Amphibian skin; Amidation; Hemolysis.

ID MOD_RES 13 13 AMIDATION.
 AC P6BA768B9DFE587D CRC64;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE NADH-UBIQUINONE OXIDOREDUCTASE 19 KD SUBUNIT (EC 1.6.5.3)
 DE (EC 1.6.99.3) (COMPLEX I-19KD) (COMPLEX I-PGIV) (CI-PGIV)
 DE (NDUFAB8).
 Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Buteraria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP
 RC TISSUE-KIDNEY;
 RX MEDLINE: 97295305.
 RA Saro C., Marocchi A., Sanchez J.-C., Giannoni B., Frutiger S.,
 RA Golaz O., Wilkins M.R., Doro G., Cappellano F., Hughes G.J.,
 RA Hochstrasser D.F., Mocarelli P.;
 RT "Renal cell carcinoma and normal kidney protein expression.";
 RL Electrophoresis 18:599-604(1997).
 CC -1- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 TO BE UBIQUINONE.
 CC -1- CATALYTIC ACTIVITY: NADH + UBIQUINONE = NAD(+)+ UBIQUINOL.
 CC -1- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 40 DIFFERENT SUBUNITS.
 CC THIS IS A COMPONENT OF THE HYDROPHOBIC FRACTION.
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL.
 CC -1- SIMILARITY: BELONGS TO THE COMPLEX I 19 KD SUBUNIT FAMILY.
 CC SWISS-2DPAGE; P51970; HUMAN.
 DR MTM: 603359;
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 SQ

Query Match Score 48.5%; Pred. No. 8.4e+02; Length 13;
 Best Local Similarity 50.0%; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GILE 5
 Db 2 GIVE 5

RESULT 4
 ID YGDR_THEAC STANDARD; PRT; 14 AA.
 AC Q05213;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE HYPOPOETICAL PROTEIN IN GLUCOSE DEHYDROGENASE GENE 3 REGION
 DE (FRAGMENT).
 OS Thermoplasma acidophilum.
 OC Archaea; Euryarchaeota; Thermoplasmae; Thermoplasma.
 OC Thermoplasma.

RN [1]	SEQUENCE FROM N.A.	ID TRP5_LEUMA	STANDARD;	PRT;	10 AA.
RP STRAIN=DSM 1728.	AC P81737;	DT 15-FEB-2000 (Rel. 39, Created)			
RC MEDLINE; 93170285.	DT 15-FEB-2000 (Rel. 39, Last sequence update)				
RA Bright J.R., Byron D., Danson M.J., Hough D.W., Towner P.;	DT 15-FEB-2000 (Rel. 39, Last annotation update)				
RT "Cloning, sequencing and expression of the gene encoding glucose dehydrogenase from the thermophilic archaeon Thermoplasma acidophilum.";	DE TACHYKININ-RELATED PEPTIDE 5 (LEMPTR 5).				
RT Leucophaea maevae (Madeira cockroach).	OS Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea; Blaberidae; Leucophaea.				
CC	OC				
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	CC	RN [1]			
CC	DR EMBL; 259788; CAN42451.1; -.	RP PIR; S29789; S29789.	RP SEQUENCE, AND MASS SPECTROMETRY.		
CC	ENT NON_TER 14 AA; 1674 MW; 685A1FFF26529944 CRC64;	RC TISSUE-BRAIN;			
SEQUENCE	SQ	RX MEDLINE; 97269266.			
RT	RA Muren J.E., Naessel D.R.;				
RT	RT "Isolation of five tachykinin-related peptides isolated from the midgut of the cockroach Leucophaea madera: existence of N-terminally extended isoforms."				
RT	RT Regul. Pept. 65:185-196(1996).				
RT	RN [2]				
RT	RP SPOTTEST.				
RT	RC TISSUE-MIDGUT;				
RT	RX MEDLINE; 97053012.				
RT	RA Muren J.E., Naessel D.R.;				
RT	RT "Isolation of five tachykinin-related peptides isolated from the brain of the madeira cockroach: evidence for tissue-specific expression of the isoforms."				
RT	RT Peptides 18:7-15(1997).				
RT	CC -1-FUNCTION: MYOACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.				
RT	CC -1-TISSUE SPECIFICITY: MIDGUT AND BRAIN.				
RT	CC -1-MASS SPECTROMETRY: MW1033.2; METHOD-MALDI-MS.				
RT	CC -1-SIMILARITY: SOME SIMILARITY TO TACHYKININS.				
RT	KW Tachykinin; Neuropeptide; Amidation.				
RT	MOD-RES 10 10 AMIDATION.				
RT	SQ SEQUENCE 10 AA; 1033 MW; C452CD66D9C8769D CRC64;				
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CDN2_LITGI	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CON2_LITGI	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Created)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CDN2_LITGI	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CON2_LITGI	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Created)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					
RESULT 5	Query Match Score 14; DB 1; Length 10;				
CNEUROPEPTIDE	Best Local Similarity 40.0%; Pred. No. 1.5e+03; Indels 0; Gaps 0;				
ID CNEUROPEPTIDE	Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;				
AC P56247;	Score 15; DB 1;				
DT 15-JUL-1998 (Rel. 36, Last sequence update)					
QY 3 ILERV 7					
DB 4 LKRI 8					

FT MOD_RES 1 PYRROLIDONE CARBOXYLIC ACID.
 SQ SEQUENCE 11 AA; 1199 MW; 295CBF0627741777 CRC64;
 CC RESIDUES IN CAERIDIN 1.3
 CC -1- MASS SPECTROMETRY; MW=1140; METHOD=FAB.
 CC -1- MISCELLANEOUS: THE RESULTS FOR MASS SPECTROMETRY OF CAERIDIN 1.1
 CC IS 1140 IN REF.1, REF.3 AND REF.4, WHILE IN REF.2 IT IS 1139.
 CC Amphibian skin; Amidation.
 FT MOD_RES 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1141 MW; 2822551A33772728 CRC64;

Query Match Score 42.4%; Pred. No. 2e+03; Length 11;
 Best Local Similarity 50.0%; Mismatches 1; Indels 0; Gaps 0;
 Matches 3; Conservative 2; Gaps 0;

Qy 1 QGILIER 6
 ||:
 Db 1 QGLPFR 6

RESULT 8
 CD11_LITRA STANDARD; PRT: 12 AA.
 ID CD11_LITRA; PRT: 12 AA.
 AC P56245; P81253;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CAERIDIN 1.1/2.1/3.
 OS Litoria xanthomera (Orange-thighed frog), Litoria splendida,
 Litoria gilleni, and Litoria chloris (Blue-thighed frog).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphibia;
 OC Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae; Litoria.
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC SPECIES=L_XANTHOMERA;
 RX MEDLINE: 97374000.
 RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
 RAMSAY S.L.;
 RT "New caerin antibacterial peptides from the skin glands of the
 Australian tree frog Litoria xanthomera.";
 RL Pept. Sci. 3:181-185 (1997).
 RN [2]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC SPECIES=L_SPLENDIDA; TISSUE=PAROTOID GLAND;
 RA Stone D.J.M., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. Structures of the caerins and
 caeridin 1 from Litoria splendida.";
 RT J. Chem. Soc. Perkin Trans. 1:3173-3178 (1992).
 RN [3]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC SPECIES=L_GILLENI; TISSUE=PAROTOID GLAND;
 RA Waugh R.J., Stone D.J.M., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "Peptides from Australian frogs. The structures of the caerins and
 caeridins from Litoria gilleni.";
 RL Pept. Res. 13:937-961 (1993).
 RN [4]
 RP SEQUENCE, AND MASS SPECTROMETRY (CAERIDINS 1.1, 1.2 AND 1.3).
 RC SPECIES=L_GILLENI;
 RX MEDLINE: 98175802.
 RA Steinborner S.T., Currie G.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "New antibiotic caerin 1 peptides from the skin secretion of the
 Australian tree frog Litoria chloris. Comparison of the activities of
 the caerin 1 peptides from the genus Litoria.";
 RL Pept. Res. 51:121-126 (1998).
 CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 CC ANTIBIOTIC ACTIVITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -!- MASS SPECTROMETRY: MW=1096; METHOD=FAB.
 CC Amphibian skin; Amidation.
 FT MOD_RES 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1097 MW; 28225503E3772728 CRC64;

Query Match Score 42.4%; Pred. No. 2.2e+03; Length 12;
 Best Local Similarity 50.0%; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FILE 5
 Db 1 GLDD 4

RESULT 9
 CD14_LITRA STANDARD; PRT: 12 AA.
 ID CD14_LITRA; PRT: 12 AA.
 AC P57246;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CAERIDIN 1.4.
 OS Litoria xanthomera (Orange-thighed frog), and
 Litoria chloris (Blue-thighed frog).
 OS Litoria chloris; Chordata; Craniata; Vertebrata; Amphibia;
 OC Eukaryota; Metazoa; Neobatrachia; Bufonoidea; Hylidae; Litoria.
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC SPECIES=L_XANTHOMERA;
 RX MEDLINE: 97374000.
 RA Steinborner S.T., Waugh R.J., Bowie J.H., Wallace J.C., Tyler M.J.,
 RAMSAY S.L.;
 RT "New caerin antibacterial Peptides from the skin glands of the
 Australian tree frog Litoria xanthomera.";
 RL Pept. Sci. 3:181-185 (1997).
 RN [2]
 RP SEQUENCE,
 RC SPECIES=L_CHLORIS; TISSUE=SKIN;
 RX MEDLINE: 98175802.
 RA Steinborner S.T., Currie G.J., Bowie J.H., Wallace J.C., Tyler M.J.;
 RT "New antibiotic caerin 1 peptides from the skin secretion of the
 Australian tree frog Litoria chloris. Comparison of the activities of
 the caerin 1 peptides from the genus Litoria.";
 RL Pept. Res. 51:121-126 (1998).
 CC -!- FUNCTION: CAERIDINS SHOW NEITHER NEUROPEPTIDE ACTIVITY NOR
 CC ANTIBIOTIC ACTIVITY.
 CC -!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS.
 CC -!- MASS SPECTROMETRY: MW=1096; METHOD=FAB.
 CC Amphibian skin; Amidation.
 FT MOD_RES 12 AMIDATION.
 SQ SEQUENCE 12 AA; 1097 MW; 28225503E3772728 CRC64;

Query Match Score 42.4%; Pred. No. 2.2e+03; Length 12;
 Best Local Similarity 50.0%; Mismatches 2; Indels 0; Gaps 0;

Qy 2 FILE 5
 Db 1 GLDD 4

RESULT 10
 CHEP_PARD STANDARD; PRT: 13 AA.
 ID CHEP_PARD; STANDARD; PRT: 13 AA.
 AC P4218;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)

-!- TISSUE SPECIFICITY: SECRETED BY THE SKIN DORSAL GLANDS IN L.
 CC XANTHOMERA OR SPECIFICALLY BY THE SKIN PAROVID AND/OR ROSTRAL
 GLANDS IN L. SPLENDIDA AND L. GILLENI.
 CC -!- PTM: ISOMERIZATION ALPHA-BETA OF THE ASP-4 RESIDUE IN CAERIDIN
 1.2; A CYCLIC SUCCINIMIDE MAY BE FORMED BETWEEN ASP-4 AND GLY-5

DE CHEMOTACTIC PEPTIDE.
 OS Parapolybia indicae; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Eukaryota; Metazoa; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 CC Pterygota; Neoptera; Endopterygota; Hymenoptera; Polistinae; Parapolybia.
 RN [1]
 SEQUENCE.
 RP TISSUE=VENOM;
 RA Toki T., Yashihara T., Nakajima T.;
 RT "Isolation and sequential analysis of peptides on the venom sac of
 Parapolybia indicae.";
 RL Eisei Dobutsu 39:105-111(1988).
 KW Chemotaxis; Amidation.
 FT MOD_RES 13 13 AMIDATION.
 SQ SEQUENCE 13 AA: 1298 MW: 5C90CEB39D5873 CRC64;

Query Match 42.4% Score 14; DB 1; Length 13;
 Best Local Similarity 33.3%; Pred. No. 2.4e+03;
 Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILERV 7
 Db 3 GLIKGI 8

RESULT 11
 FIBB_HYLIA ID FIBB_HYLIA STANDARD: PRT; 13 AA.
 AC P14472; DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-FEB-1994 (Rel. 28, Last annotation update)
 DE FIBRINOPEPTIDE B.
 OS Hylobates lar (Common gibbon).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hylobatidae; Hylobates.
 RN [1]
 SEQUENCE.
 RX MEDLINE: 70294424;
 RA Gross G.A., Doolittle R.F., Roberts B.F.;
 RT "Gibbon fibrinopeptides: identification of a glycine-serine alleleism
 at position B-3.";
 RL SCIENCE 170:46-47(1970).
 CC -!- FUNCTION: FIBRINOGEN HAS A DOUBLE FUNCTION: YIELDING MONOMERS THAT
 POLYMERIZE INTO FIBRIN AND ACTING AS A COFACTOR IN PLATELET
 AGGREGATION.
 CC -!- SUBUNIT: HEXAMER CONTAINING 2 SETS OF 3 NONIDENTICAL CHAINS
 (ALPHA, BETA, & GAMMA), LINKED TO EACH OTHER BY DISULFIDE BONDS.
 CC -!- MISCELLANEOUS: CONVERSION OF FIBRINOGEN TO FIBRIN IS TRIGGERED BY
 THROMBIN, WHICH CLEAVES FIBRINOPEPTIDES A AND B FROM ALPHA & BETA
 CHAINS, AND THUS EXPOSES THE N-TERMINAL POLYMERIZATION SITES
 RESPONSIBLE FOR THE FORMATION OF THE SOFT CLOT.
 CC PROSITE: PS00514; FIBRIN_{AG_C} DOMAIN; PARTIAL.
 DR Blood coagulation; Plasma.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 FT NON_TER 11 11 S->G.
 SQ SEQUENCE 13 AA: 1406 MW: 7D944D60187D698F CRC64;

Query Match 42.4% Score 14; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 2.4e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
 Db 1 QGV 3

RESULT 13
 MY14_EISFO STANDARD; PRT; 14 AA.
 ID MY14_EISFO
 AC P45979;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE MYCROATIVE TETRADECAPETIDE (ERP).
 OS Eisenia foetida (Common earthworm) (Common dung worm).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotaxida;
 Lumbricina; Lumbriidae; Eisenia.
 RN [1]
 SEQUENCE AND SYNTHESIS.
 RC TISSUE=GIT;
 RX MEDLINE: 96087879.
 RA Usena K., Onuki T., Matsushima O., Ikeda T., Fujita T., Minakata H.,
 Nomoto K.;
 RA "A novel gut tetradecapeptide isolated from the earthworm, Eisenia
 fetida.";
 RL Peptides 16:995-999(1995).
 CC -!- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF GUT
 MUSCLES.
 CC -!- SIMILARITY: TO INSECTS ALLATOTROPIN.
 KW Neuropeptide; Amidation.
 FT MOD_RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA: 1478 MW: CC9ABEF941CD91AD CRC64;

Query Match 42.4% Score 14; DB 1; Length 14;
 Best Local Similarity 33.3%; Pred. No. 2.4e+03;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 QGI 3
 Db 1 QGV 3

RESULT 12
 FIBB_MANLE STANDARD;
 ID FIBB_MANLE

Qy	2 GILERV 7 : : Db	5 GADRI 10	Query Match Best Local Similarity 50.0%; Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
RESULT 14			
UN37_CLOPA	STANDARD;	PRT;	14 AA.
AC P81358;			
DT 15-JUL-1998 (Rel. 36; Created)			
DT 15-JUL-1998 (Rel. 36; Last sequence update)			
DE UNKNOWN PROTEIN CP 37 FROM 2D-PAGE (FRAGMENT).			
OS Clostridium pasteurianum.			
Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridiaceae;			
Clostridium.			
[1]			
RP SEQUENCE;			
RC STRAIN=W5;			
RX MEDLINE; 98291670.			
RA Flengsrød R., Skjelstad L.;			
RT "Two-dimensional gel electrophoresis separation and N-terminal			
RT sequence analysis of proteins from Clostridium pasteurianum W5.";			
RL Electrophoresis 19:802-806(1998).			
CC -I- MISCELLANEOUS: ON THE 2D-CEL THE DETERMINED PI OF THIS UNKNOWN			
PROTEIN IS: 5.8, ITS MW IS: 44.7 KD.			
FT NON-TER 14 AA; 14 1579 MW; 05384662DEF89210 CRC64;			
SQ SEQUENCE 14 AA; 15 AA; 1579 MW; 05384662DEF89210 CRC64;			
Query Match Best Local Similarity 42.4%; Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;			
Score 14; DB 1; Length 14;			
Qy 1 QGI 3 : : Db 10 QGV 12			
RESULT 15			
LPL_THETH	STANDARD;	PRT;	15 AA.
AC P21234;			
DT 01-MAY-1991 (Rel. 18; Created)			
DT 01-MAY-1991 (Rel. 18; Last sequence update)			
DT 01-MAY-1991 (Rel. 18; Last annotation update)			
DE LEU LEADER PEPTIDE.			
OS Thermus aquaticus (subsp. thermophilus).			
OC Bacteria; Thermus/Deinococcus group; Thermus group; Thermus.			
RN [1]			
RP SEQUENCE FROM N.A.			
RC STRAIN=HBB;			
RX MEDLINE; 88121725;			
RA Croft J.E., Love D.R., Bergquist P.L.;			
RT "Expression of leucine genes from an extremely thermophilic bacterium			
in Escherichia coli".			
RL Mol. Gen. Genet. 210:490-497(1987).			
CC -I- FUNCTION: THIS PROTEIN IS INVOLVED IN CONTROL OF THE BIOSYNTHESIS			
OF LEUCINE.			
CC This SWISS-PROT entry is copyright. It is produced through a collaboration			
between the Swiss Institute of Bioinformatics and the EMBL outstation -			
the European Bioinformatics Institute. There are no restrictions on its			
use by non-profit institutions as long as its content is in no way			
modified and this statement is not removed. Usage by and for commercial			
entities requires a license agreement (see http://www.isb-sib.ch/announce/			
CC or send an email to license@isb-sib.ch).			
CC DR EMBL; X06604; CAA29833.1;			
DR PIR; S0090.; LFTWL.			
KW Leader Peptide; Leucine biosynthesis.			
SQ SEQUENCE 15 AA; 1666 MW; C2F10/A386D7620B CRC64;			
Query Match Best Local Similarity 42.4%; Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;			
Qy 3 ILER 6 : : Db 8 VLDR 11			
RESULT 16			
MALT_BACTQ	STANDARD;	PRT;	15 AA.
ID P80772;			
AC P80772; (Rel. 23; Created)			
DT 01-AUG-1992 (Rel. 23; Last sequence update)			
DT 01-AUG-1992 (Rel. 23; Last annotation update)			
DT 01-DEC-1992 (Rel. 24; Last annotation update)			
DE MALTASE (EC 3.2.1.10) (ALPHA-GLUCOSIDASE 1) (FRAGMENT).			
OS Bacillus thermomyoliiquefaciens.			
OC Bacteria; Firmicutes; Bacilli/Clostridium group;			
OC Bacillus/Staphylococcus group; Bacillus.			
OC [1]			
RN SEQUENCE.			
RP STRAIN=KP1071 / FERM P8477;			
RC MEDLINE; 9220510.			
RA Suzuki Y., Yonezawa K., Hattori M., Takii Y.;			
RT Assignment of Bacillus thermomyoliiquefaciens KP1071 alpha-glucosidase I to an exo-alpha-1,4-glucosidase, and its striking similarity to bacillary oligo-1,6-glucosidases in N-terminal sequence composition."			
RT parameters calculated from the amino acid composition."			
RT Eur. J. Biochem. 205:249-256(1992).			
RT -I- CATALYTIC ACTIVITY: HYDROLYSIS OF TERMINAL, NON-REDUCING			
RT -I- LINKED D-GLUCOSE RESIDUES WITH RELEASE OF D-GLUCOSE.			
CC -I- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO			
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.			
DR PIR: S21240; S21240.			
KW Hydrolase; Glycosidase.			
FT NON-TER 15 AA; 15 MW; 62B4CE501F2D3042 CRC64;			
SQ SEQUENCE 15 AA; 15 MW; 62B4CE501F2D3042 CRC64;			
Query Match Best Local Similarity 42.4%; Matches 1; Conservative 1; Mismatches 5; Indels 1; Gaps 0;			
Score 14; DB 1; Length 15;			
Qy 1 QGILERV 7 : : Db 8 EGVVYQI 14			
RESULT 17			
PA2B_VIPBO	STANDARD;	PRT;	12 AA.
ID P3159;			
AC P3159; (Rel. 26; Created)			
DT 01-JUL-1993 (Rel. 26; Last sequence update)			
DT 01-JUL-1993 (Rel. 26; Last annotation update)			
DE PHOSPHOLIPASE A2, BASIC (EC 3.1.1.4) (PHOSPHATIDYLCHOLINE			
DE 2-ACETYLYDROLASE (FRAGMENT).			
OS Vipera berus orientalis (Viper).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Lepidosauria;			
OC Squamata; Scincoglossa; Serpentes; Colubroidea; Viperidae; Viperinae;			
OC Vipera.			
RN [1]			
RP SEQUENCE-VENOM.			
RC MEDLINE; 74120698.			
RA Deloisi P.J.;			
RT "purification and physicochemical, chemical and biological properties			
of a toxic A2 phospholipase isolated from the venom of viperidae			
RT snakes: Vipera berus".			
RL Biochimie 55:1031-1045(1973).			

CC -!- FUNCTION: PA2 CATALYZES THE CALCIUM-DEPENDENT HYDROLYSIS OF THE
 CC 2-ACYL GROUPS IN 3-SN-PHOSPHATIDYLGlycerol + H(2)O = 1-ACYLGLYCERYL-
 CC -!- CATALYTIC ACTIVITY: PHOSPHATIDYLGlycerol + H(2)O = 1-ACYLGLYCERYL-
 CC PHOSPHOCHOLINE + A FATTY ACID ANION.
 CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY.
 DR PROSITE; PS00118; PA2_HIS; PARTIAL.
 DR PROSITE; PS00119; PA2_ASP; PARTIAL.
 KW Hydrolase; Lipid degradation; Calcium; Venom.
 FT NON_TER 12 12
 SEQUENCE 12 AA; 1412 MW; D054351A89965879 CRC64;
 Query Match 39.4%; Score 13; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 ILE 5
 |||
 Db 9 ILE 11

RESULT 18
 UP01_CABEL STANDARD PRT; 12 AA.
 ID UP01_CABEL STANDARD PRT; 12 AA.
 AC P55954;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE (SPOT 1) (FRAGMENT).
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Secernentea; Rhabditida; Rhabditina; Rhabditoidae; Rhabditidae; Peioderinae; Caenorhabditis.
 RN [1]
 RP SEQUENCE.
 RC STRAIN=BRISTOL N2;
 RX MEDLINE; 97295299;
 RA Bini L., Heid H., Liberatori S., Geier G., Pallini V., Zwilling R.;
 RT homogenates and gel electrophoresis of *caenorhabditis elegans*
 RT homogenates and identification of protein spots by microsequencing ";
 RL Electrophoresis 18:557-562(1997).
 FT NON_TER 12 12
 SEQUENCE 12 AA; 1409 MW; 8DC4A7105316905A CRC64;

Query Match 39.4%; Score 13; DB 1; Length 12;
 Best Local Similarity 50.0%; Pred. No. 3.7e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 SQ 3 ILE 6
 |||:
 Db 6 IMPR 9

RESULT 19
 CRBL_VESCR STANDARD PRT; 13 AA.
 ID CRBL_VESCR STANDARD PRT; 13 AA.
 AC P01518;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE CRABROLIN.
 OS Vespa crabro (European hornet).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Vespoidea; Vespidae; Vespinae; Vespa.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=VENOM;
 RX MEDLINE; 8429390.
 RA Argiolas A., Pisano J.J.;
 RT Isolation and characterization of two new peptides, mastoparan C and
 RT crabrolin, from the venom of the European hornet, *Vespa crabro*.";
 RL J. Biol. Chem. 259:10106-10111(1984).

RN [2] SYNTHESIS, AND ANTIMICROBIAL ACTIVITY.
 RP MEDLINE; 97119326.
 RX Krishnakumari V., Nagaraj R.;
 RA Krishnakumari V., Nagaraj R.;
 RT "Antimicrobial and hemolytic activities of crabrolin, a 13-residue peptide from the venom of the European hornet, *Vespa crabro*, and its analogs.";
 RT J. Pept. Res. 50:88-93(1997).
 RL CC -!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE INDUCES THE CHEMOTAXIS OF NEUTROPHILS. HAS ANTIMICROBIAL AND HEMOLYTIC ACTIVITY.
 CC PIR; A01781; JZVHP1.
 KW Mast cell degranulation; Chemotaxis; Venom; Amidation; Antibiotic.
 FT MOD_RES 13 13
 SQ SEQUENCE 13 AA; 1457 MW; 515EF8FCFA8D2407 CRC64;
 Query Match 39.4%; Score 13; DB 1; Length 13;
 Best Local Similarity 40.0%; Pred. No. 4e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 3 ILERV 7
 |||:
 Db 5 ILRKI 9

RESULT 20
 FAB2_ASGSU STANDARD PRT; 13 AA.
 ID FAB2_ASGSU STANDARD PRT; 13 AA.
 AC P43173;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE FMRFamide-like neuropeptide AF11.
 OS Ascaris suum (Pig roundworm) (*Ascaris lumbricoides*).
 OC Eukaryota; Metazoa; Secernentea; Rhabditia; Ascaridida; Ascaris.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 95180362.
 RA Conden C., Stretton A.O.W.;
 RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode *Ascaris suum*";
 RT Peptides 16:491-500(1995).
 -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE) FAMILY.
 CC FAMILY.
 KW Neuropeptide; Amidation.
 FT MOD_RES 13 13
 SQ SEQUENCE 13 AA; 1495 MW; 9CAEC650D6886B05 CRC64;
 Query Match 39.4%; Score 13; DB 1; Length 13;
 Best Local Similarity 75.0%; Pred. No. 4e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GILE 5
 |||:
 Db 4 GISE 7

RESULT 21
 HP9_RANES STANDARD PRT; 13 AA.
 ID HP9_RANES STANDARD PRT; 13 AA.
 AC P34416;
 DT 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE HELIOTIC PROTEIN B9 (FRAGMENT).
 OS Rana esculenta (Edible frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Amphia;
 OC Batrachia; Anura; Neobatrachia; Ranidae; Ranidae; Raninae; Rana.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=SKIN SECRETION;

RX MEDLINE: 90198965.
 RA Simmaco M., de Biase D., Severini C., Aita M., Erspaner G.F.,
 RA Barra D., Bossa F.;
 RT "Purification and characterization of bioactive peptides from skin
 extracts of Rana esculenta.",
 RL Biochim. Biophys. Acta 1033:318-323(1990).
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- TISSUE SPECIFICITY: SKIN.
 DR PIR: S09019; S09019
 KW Amphibian skin; Amidation; Hemolysis.
 FT MOD-RES 13 13 AMIDATION.
 FT NON-TER 13 13
 SQ SEQUENCE 13 AA; 1402 MW; C6B4A1A765DF9287D CRC64;

Query Match 39.4%; Score 13; DB 1; Length 13;
 Best Local Similarity 33.3%; Pred. No. 4e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GILERY 7
 Db 1 :| :| :| :| 12
 7 GLGRL 12

RESULT 22
 CRBL_VESOR STANDARD; PRT; 14 AA.
 ID CRBL_VESOR
 AC P17236;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 01-AUG-1990 (Rel. 15, Last annotation update)
 DE HISTAMINE RELEASING PEPTIDE II (HR-II).
 OS Vespa orientalis (Oriental hornet).
 EC 146-147(1981).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata.
 OC Vespidae; Vespidae; Vespinae; Vespa.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=VENOM;
 RA Miroshnikov A. I., Snejhrova L.G., Nazzimov I.V., Reshetova O. I.,
 RA Rozynov B.V., Gushchin I.S.;
 RT "Structure and properties of histamine releasing peptides from the
 venom of Vespa orientalis hornet.";
 RL Bioorg. Khim. 7:146-147(1981).
 CC -!- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS
 OF NEUTROPHILS.
 DR JN0380; JN0390.
 KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
 FT MOD-RES 14 14 AMIDATION.
 SQ SEQUENCE 14 AA; 1524 MW; 22015B4A5CFDF38 CRC64;

Query Match 39.4%; Score 13; DB 1; Length 14;
 Best Local Similarity 50.0%; Pred. No. 4.3e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QGIL 4
 Db 1 :| :| 11 KGLL 14

RESULT 23
 IF2G_RAT STANDARD; PRT; 14 AA.
 ID IF2G_RAT
 AC P81795;
 DT 15-FBB-2000 (Rel. 39, Created)
 DT 15-FBB-2000 (Rel. 39, Last sequence update)
 DT 15-FBB-2000 (Rel. 39, Last annotation update)
 DE EUKARYOTIC TRANSLATION INITIATOR FACTOR 2 GAMMA SUBUNIT (EIF-2-
 DE GAMMA) (PP42) (FRAGMENT).
 GN EIF2S3 OR EIF2G.
 OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sclerognathii; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=LIVER;
 RX MEDLINE; 96374441.
 RA G11 C., Plana M., Riera M., Itarte E.;
 RT CK2, is composed of the beta and the gamma subunits of translation
 initiation factor eIF-2.;
 RL Biochem. Biophys. Res. Commun. 225:1052-1057(1996).
 CC -!- FUNCTION: EIF-2 FUNCTIONS AS THE EARLY STEPS OF PROTEIN SYNTHESIS
 BY FORMING A TERNARY COMPLEX WITH GTP AND INITIATOR tRNA. THIS
 COMPLEX BINDS TO A 40S RIBOSOMAL SUBUNIT, FOLLOWED BY mRNA BINDING
 TO FORM A 43S PREINITIATION COMPLEX. JUNCTION OF THE 60S RIBOSOMAL
 SUBUNIT TO FORM THE 80S INITIATION COMPLEX IS PRECEDED BY
 HYDROLYSIS OF THE GTP BOUND TO EIF-2 AND RELEASE OF AN EIF-2-GDP
 BINARY COMPLEX. IN ORDER FOR EIF-2 TO RECYCLE AND CATALYZE ANOTHER
 ROUND OF INITIATION, THE GDP BOUND TO EIF-2 MUST EXCHANGE WITH GTP
 BY WAY OF A REACTION CATALYZED BY EIF-2B.
 CC -!- SUBUNIT: HETEROTRIMERIC COMPOSED OF AN ALPHA, A BETA, AND A GAMMA
 CHAIN.
 CC -!- SIMILARITY: TO GTP-DEPENDENT ELONGATION FACTORS.
 KW Initiation factor; Protein biosynthesis; GTP-binding.

Query Match 39.4%; Score 13; DB 1; Length 14;
 Best Local Similarity 40.0%; Pred. No. 4.3e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GILER 6
 Db 1 :| :| 10 GIVSK 14

RESULT 24
 MY14_PHEV1 STANDARD; PRT; 14 AA.
 ID MY14_PHEV1
 AC P46180;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE MYCOTIVE TETRADECAPEPITIDE (PTP).
 OS Pherotima vittata (Earthworm).
 OC Lumbricina; Metazoa; Annelida; Clitellata; Oligochaeta; Haplotauxia.
 OC Megascolecidae; Pherotima.
 RN [1]
 RP SEQUENCE, AND SYNTHESIS.
 RC TISSUE=GUT;
 RX MEDLINE; 96087879.
 RA Ueda K., Oumi T., Matsushima O., Ikeda T., Minakata H.,
 RA Nomoto K.;
 RT "A novel gut tetradecapeptide isolated from the earthworm, Eisenia
 fetida.";
 RL Peptides 16:995-999(1995).
 CC -!- FUNCTION: HAS A STIMULATIVE EFFECT ON THE CONTRACTION OF CUT
 CC MUSCLES.
 CC -!- SIMILARITY: TO INSECTS ALLATOTROPIN.
 KW Neuropeptide; Amidation.
 FT MOD-RES 14 14 AMDATATION.
 SQ SEQUENCE 14 AA; 1522 MW; DA40BEE67CCD91AD CRC64;

Query Match 39.4%; Score 13; DB 1; Length 14;
 Best Local Similarity 33.3%; Pred. No. 4.3e+03;
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 GILER 7
 Db 1 :| :| 5 GSADRI 10

RESULT 25
 ACPH_RABBIT STANDARD; PRT; 6 AA.
 ID P25154; Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 01-OCT-1995 (Rel. 34, Last annotation update)
 DE ACYLAMINO ACID-RELEASING ENZYME (EC 3.4.19.1) (ACYL-PEPTIDE HYDROLASE)
 DE (APEH)
 GN (ACPHEH)
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Lagomorpha; Leporidae; Oryctolagidae.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-MUSCLE;
 RX MEDLINE; 92222120.
 RA Krishna R.G., Chin C.C.-Q., Wold F.;
 RT "N-terminal sequence analysis of N alpha-acetylated proteins after
 unblocking with N-acylaminocycl-peptide hydrolase.";
 RT Anal. Biochem. 199 45-50(1991).
 -: FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
 TERMINAL PEPTIDE BOND OF N ACETYLATED PEPTIDE TO GENERATE
 AN ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
 CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
 CC -1- CATALYTIC ACTIVITY: ACYLAMINOACYL-PEPTIDE + H(2)O = ACYLAMINO
 CC ACID + PEPTIDE.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C; ALSO KNOWN AS THE
 PROLINE OLIGOPEPTIDASE FAMILY.
 DR PS007008; PRO-ENDOPEPF SER; PARTIAL.
 KW Hydro-lase; Acetylation.
 FT MOD-RES 1 1 ACETYLATION.
 FT NON-TER 6 6
 SEQUENCE 6 AA; 775 MW; 6732D6C40B16F000 CRC64;
 Query Match 36.4%; Score 12; DB 1; Length 6;
 Best Local Similarity 66.7%; Pred. No. 8.4e+04; 0; Indels 0; Gaps 0;
 Matches 2; Conservative 1; Mismatches 0; Standard; PRT; 10 AA.

RESULT 26
 CU30_LOCMI STANDARD; PRT; 10 AA.
 ID P11735;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE CUTICLE PROTEIN 30 (LM-ACP 30) (FRAGMENT).
 OS Locusta migratoria (Migratory locust).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
 OC Acridoidea; Acridoidea; Acrididae; Oedipodinae; Locusta.
 RN [1]
 RP SEQUENCE. MEDLINE: 86108304.
 RA Hoeijrup P., Andersen S.O., Roepstorff P.;
 RT "Isolation, characterization, and N-terminal sequence studies of cuticular proteins from the migratory locust, *Locusta migratoria*.";
 RL Eur. J. Biochem. 154:153-159 (1986).
 CC -1- FUNCTION: COMPONENT OF THE CUTICLE OF MIGRATORY LOCUST WHICH
 CONTAINS MORE THAN 100 DIFFERENT STRUCTURAL PROTEINS.
 DR PIR: C24802; C24802.
 RW Structural protein; Cuticle.
 FT NON-TER 10 10
 SEQUENCE 10 AA; 969 MW; 4973E36B5872877 CRC64;

Query Match 36.4%; Score 12; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 5.2e+03; 0; Indels 0; Gaps 0;
 Matches 2; Conservative 1; Mismatches 0; Standard; PRT; 10 AA.

RESULT 27
 TRP9 LEUTMA STANDARD; PRT; 10 AA.
 ID P81741;
 AC 15-FEB-2000 (Rel. 39, Created)
 DT 15-FEB-2000 (Rel. 39, Last sequence update)
 DT 15-FEB-2000 (Rel. 39, Last annotation update)
 DE TACHYKININ-RELATED PEPTIDE 9 (LENTRP 9).
 OS Leucophaea maderae (Madeira cockroach).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
 OC Blaberoidea; Blaberidae; Leucophaea.
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=RAIN MEDLINE: 97269266.
 RA Muren J.E., Næsset D.R.;
 RT "Seven tachykinin-related peptides isolated from the brain of the madeira cockroach; evidence for tissue-specific expression of isoforms.";
 RT Peptides 18:7-15(1997).
 -: FUNCTION: INACTIVE PEPTIDE. INCREASES THE AMPLITUDE AND FREQUENCY OF SPONTANEOUS CONTRACTIONS AND TONUS OF HINDGUT MUSCLE.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- MASS SPECTROMETRY: MW=1081.5; METHOD=MALDI-MS.
 CC -1- SIMILARITY: SOME SIMILARITY TO TACHYKININS.
 KW Tachykinin; Neuropeptide; Amidation.
 FT MOD-RES 10 10 AMIDATION.
 SQ SEQUENCE 10 AA; 1081 MW; 9E469D66D9C87685 CRC64;

Query Match 36.4%; Score 12; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 5.2e+03; 0; Indels 0; Gaps 0;
 Matches 2; Conservative 1; Mismatches 0; Standard; PRT; 10 AA.

RESULT 28
 URAL_HUMAN STANDARD; PRT; 10 AA.
 ID P34118;
 AC 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-JUL-1998 (Rel. 36, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF RED BLOOD CELLS (SPOT 1) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=ERYTHROCYTE; MEDLINE: 94147970.
 RA Golaz O., Hughes G.J., Frutiger S., Paquet N., Bairoch A.,
 RA Pasquali C., Sanchez J.-C., Tissot J.-D.; Appel R.D., Walzer C.,
 RA Balant L., Hochstrasser D.F.;
 RT "Plasma and red blood cell protein maps: update 1993.";
 RL Electrophoresis 14:1223-1231(1993).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 5.4, ITS MW IS: 23 KD.
 CC

DR SWISS-2DPAGE; P32118; HUMAN.
 FT NON-TER 1 1
 FT 10 10
 SQ SEQUENCE 10 AA; 977 MW; 723C65B1ADD0587B CRC64;

Query Match Score 12; DB 1; Length 10;
 Best Local Similarity 66.7%; Pred. No. 5.2e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 QGI 3
 :1:
 Db 3 EGI 5

RESULT 29
 CH60_DROME STANDARD PRT; 11 AA.
 ID CH60_DROME
 AC P35310; (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE MITOCHONDRIAL MATRIX PROTEIN P1 (60 kD CHAPERONIN) (HEAT SHOCK PROTEIN 60) (HSP-60) (PROTEIN CPN60) (GROEL PROTEIN) (FRAGMENT).
 GN MMP-PL OR HSP60
 OS Drosophila melanogaster (Fruit fly).
 OC Metazoa; Neoptera; Endopterygota; Tracheata; Hexapoda; Insecta;
 OC Ephydriidae; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE.

STRAN=VALLECAS; TISSUE=WING IMAGINAL DISK;
 RX 93272852.
 RA Santaren J.F., van Damme J., Puype M., Vandekerckhove J.,
 RA Garcia-Bellido A.;
 RT "Identification of Drosophila wing imaginal disc proteins by two-dimensional gel analysis and microsequencing.";
 RL Exp. Cell Res. 206:220-226(1993).

CC -1- FUNCTION: IMPLICATED IN MITOCHONDRIAL PROTEIN IMPORT AND MACROMOLECULAR ASSEMBLY. MAY FACILITATE THE CORRECT FOLDING OF IMPORTED PROTEINS. MAY ALSO PREVENT MISFOLDING AND PROMOTE THE REFOLDING AND PROPER ASSEMBLY OF UNFOLDED POLYPEPTIDES GENERATED UNDER STRESS CONDITIONS IN THE MITOCHONDRIAL MATRIX (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE CHAPERONIN (HSP60) FAMILY.
 DR FLYBASE: FBgn0010375; MNP-P1.
 DR PRO236; CHAPERONINS_CPN60; PARTIAL.
 KW Chaperone; ATP-binding; Mitochondrion.
 FT NON-TER 1 1
 FT 11 11
 SQ SEQUENCE 11 AA; 1243 MW; 78501A366365A6DB CRC64;

OC Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata;
 OC Vespoidea; Vespidae; Polistinae; Icaria.
 RN [1]
 RP SEQUENCE.
 RC TISSUE=VENOM;
 RA Yashihara T., Itokawa H., Suzuki N., Nakamura H., Nakajima T.;
 RL (In) Izumiya N. (eds.); Peptide Chemistry 1984; pp.177-182, Protein Research Foundation, Osaka (1985).
 CC -1- FUNCTION: MAST CELL DEGRANULATING PEPTIDE. INDUCES THE CHEMOTAXIS OF NEUTROPHILS.
 KW Mast cell degranulation; Chemotaxis; Venom; Amidation.
 FT MOD_RES 13 AMIDATION.
 SQ SEQUENCE 13 AA; 1353 MW; 348DBC7A30A3768 CRC64;

Query Match Score 12; DB 1; Length 13;
 Best Local Similarity 66.7%; Pred. No. 6.7e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GIL 4
 :1:
 Db 10 GLL 12

Search completed: June 30, 2000, 19:03:16
 Job time: 15039 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 30, 2000, 16:18:45 ; search time 53.11 seconds
(without alignments)
9.138 Million cell updates/sec

Title: US-08-833-506c-120
Perfect score: 33
Sequence: 1 QGTLERV 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 1120

Minimum DB seq length: 0
Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : SPTRIMBL_12.*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rhodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB	ID	Description
1	19	57.6	11	2	044237		044237 anabena sp
2	19	57.6	15	2	Q54325		Q54325 staphylococ
3	17.5	53.0	14	2	O10334		O10234 human immun
4	17	51.5	13	2	P74844		P78444 salmorella
5	17	51.5	13	4	Q16406		Q16406 homo sapien
6	16	48.5	11	7	Q77910		Q77910 oreochromis
7	16	48.5	12	2	Q53183		Q53183 rhodococcus
8	16	48.5	13	4	Q16007		Q16007 homo sapien
9	16	48.5	15	12	Q97050		Q97050 human immun
10	15	45.5	10	2	Q9X3M2		Q9X3M2 prochloroco
11	15	45.5	10	13	Q73394		Q73394 gallus gallus
12	15	45.5	12	5	Q9X956		Q9X956 streptomyce
13	15	45.5	11	7	Q77911		Q77911 oreochromis
14	15	45.5	13	2	Q9X3J6		Q9X3J6 prochloroco
15	15	45.5	13	3	Q9X3E1		Q9X3E1 prochloroco
16	15	45.5	13	3	P87031		P87031 saccharomyces
17	15	45.5	15	10	Q65177		Q65177 mesembryant
18	15	45.5	15	12	Q97052		Q97052 human immun
19	15	45.5	15	12	Q97094		Q97094 human immun
20	14.5	43.9	14	12	O10226		O10226 human immun

21	14.5	43.9	12	12	O10227	human immun
22	14.5	43.9	14	12	O10228	human immun
23	14.5	43.9	14	12	O10229	human immun
24	14.5	43.9	14	12	O10230	human immun
25	14.5	43.9	12	12	O10232	human immun
26	14.5	43.9	14	12	O10233	human immun
27	14.5	43.9	14	12	O10235	human immun
28	14	42.4	8	6	Q28866	megaptera n
29	14	42.4	9	4	Q15892	homo sapien
					P77484	homo sapien
					P60192	spiroplasma
					Q55094	synchocystis
					Q60194	spiroplasma
					Q54861	streptococc
					Q5837	rhizobium l
					Q64971	alfalfa mos
					Q46039	citrobacter
					Q53358	escherichia
					Q79359	human immun
					Q97098	human immun
					Q9XK1	prochloroco
					Q14342	homo sapien
					Q46013	caulobacter
					Q78794	pyelella l
					Q15997	homo sapien
					P97134	rhizobium l
					Q10421	influenza a
					Q47601	escherichia
					P92076	euhada her
					Q10231	human immun
					Q69173	yersinia pe
					Q52640	pseudomonas
					Q66113	cherry leaf escherichia
					Q51594	escherichia
					Q64024	mus musculu
					Q64025	mus spreitus
					Q95574	homo sapien
					Q84333	simian virus
					Q25355	locusta mig
					Q23356	locusta mig
					Q77871	oreochromis
					Q77872	oreochromis
					Q77873	oreochromis
					Q83083	leucania sce
					Q46664	macropodus ro
					Q14894	homo sapien
					Q47335	escherichia
					Q9ZB42	streptococc
					Q9x115	campylobact
					Q26075	psammochinus
					Q9XN9	campylobact
					Q52059	salmonella s
					Q97430	drosophila
					Q35911	salmo salar
					Q85713	ios sarcos
					Q45889	clostridium
					Q16468	homo sapien
					Q29810	homo sapien
					Q45057	triticum ae
					Q83977	influenza a
					Q1069	canine dist
					Q6645	human herpe
					Q83622	murray vali
					Q85723	simian sarc

94 11 33..3 10 8 Q35013 meloidogyne
95 11 33..3 10 8 Q9XMB4 aegilops sq
96 11 33..3 11 2 Q47604 escherichia
97 11 33..3 11 2 P71228 escherichia
98 11 33..3 11 4 Q16217 homo sapien
99 11 33..3 11 4 Q94785 homo sapien
100 11 33..3 11 11 Q62207 mus musculus

ALIGNMENTS

RESULT 1
Q44237 PRELIMINARY; PRT; 11 AA.
ID Q44237;
AC 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
DE GLUTAMINE SYNTHETASE (FRAGMENT).
GN GLNA.
OS Anabaena sp.
OC Cyanobacteria; Nostocales; Nostocaceae; Anabaena .
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7120;
RA WARRER L.B., LIGON P.J., STRABEL A.W., CURTIS S.E.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=PCC 7120;
RA SCAPPINO L.A.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
DR U21853; AAA65652.1; -.
FT NON-TER 11 11
SQ SEQUENCE 11 AA; 1316 MW; 0427DF84 CRC32;

Query Match 57.6%; Score 19; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 4.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 QGILERV 7
| :|:
Db 5 QEVRK 11

RESULT 2
Q54325 PRELIMINARY; PRT; 15 AA.
ID Q54325;
AC 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
DE CHLORAMPHENICOL ACETYLTRANSFERASE (FRAGMENT).
GN CAT.
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacilli; Clostridium group;
OC Staphylococcus group; Staphylococcus .
RN [1]
RP SEQUENCE FROM N.A.

STRAIN=PEW6;
RX MEDLINE; 96279895.
RA LODDER G., SCHWARZ S., GREGORY P., DYKE K.;
RT "Tandem duplication in ermC translational attenuator of the macrolide-
lincosamide-streptogramin B resistance plasmid PSE56 from
Staphylococcus equorum.";
RT Antimicrob Agents Chemother. 40:215-217(1996).
RL EMBL; X28666; CAA57981.1; -.
KW Transferase.
FT NON-TER 1 1931 MW; 996BDE4C CRC32;
SQ SEQUENCE 15 AA; 1931 MW; 996BDE4C CRC32;

035013 meloidogyne
Q9xmb4 aegilops sq
Q47604 escherichia
P71228 escherichia
Q16217 homo sapien
Q94785 homo sapien
Q62207 mus musculus

ALIGNMENTS

RESULT 3
O10234 PRELIMINARY; PRT; 14 AA.
ID O10234;
AC 010234;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DE ENVLOPE GLYCOPROTEIN (FRAGMENT).
GN Human immunodeficiency virus type 1.
OS Viruses; Retroviridae; Lentiviridae; Lentivirus.
OC [1]
RN RP SEQUENCE FROM N.A.
RX MEDLINE; 98216723.
RA SALVI R., GARBUGLIA A.R., DI CARO A., PULTANI S., MONTELLA F.,
RA BENEDETTO A.;
RA "Grossly defective nef gene sequences in a human immunodeficiency virus type 1-seropositive long-term nonprogressor.";
RL J. Virol. 72:3646-3657(1998).
DR EMBL; US9854; AAC26093.1; -.
DR PFAM; PF00517; GP41; 1.
KW Envelope protein.

FT NON-TER 1 1
SQ SEQUENCE 14 AA; 1733 MW; CBF88541 CRC32;

Query Match 57.6%; Score 19; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 1.3e+03;
Matches 3; Conservative 3; Mismatches 0; Indels 1; Gaps 1;

Qy 1 QGILERV 7
| :|:
Db 7 QG-LERI 12

RESULT 4
P74844 PRELIMINARY; PRT; 13 AA.
ID P74844;
AC P74844;
DT 01-FEB-1997 (TREMBLrel. 02, Created)
DT 01-NOV-1998 (TREMBLrel. 02, Last sequence update)
DE SIGMA FACTOR (FRAGMENT).
GN FLIA.
OS *Salmonella typhimurium*
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC *Salmonella*.
RN RP SEQUENCE FROM N.A.
RX MEDLINE; 97311993
RA NICOLLET J.;
RA BURNENS A.P., STANLEY J., SACK R., HUNZIKER P., BRODARD I.,
RC STRAIN=M-168-94;
RA "The flagellin N-methylase gene flib and an adjacent serovar-specific IS200 element in *Salmonella typhimurium*.";
RT Microbiology 143:1539-1547(1997).
RL EMBL; 267749; CAA91563.1; -.
DR FT NON-TER 13
SQ SEQUENCE 13 AA; 1459 MW; 0D3A47E3 CRC32;

Query Match 51.5%; Score 17; DB 2; Length 13;
Best Local Similarity 16.7%; Pred. No. 1.6e+03;

Query	Matches	1;	Conservative	5;	Mismatches	0;	Indels	0;	Gaps	0;	Qy	2 GILERV 7
OY	1	QGILER 6									Db	1 GFLEYI 6
Db	8	EGYMDK 13										
RESULT	5										RESULT	7
Q16406											Q53183	PRELIMINARY;
ID	Q16406;										ID	Q53183;
AC	Q16406;										AC	Q53183;
DT	01-NOV-1996	(TREMBLrel.	01; Created)								DT	01-NOV-1996 (TREMBLrel.
DT	01-NOV-1996	(TREMBLrel.	01; Last sequence update)								DT	01-NOV-1996 (TREMBLrel.
DT	01-NOV-1999	(TREMBLrel.	10; Last annotation update)								DT	01-NOV-1999 (TREMBLrel.
DE	GHRH-R PROTEIN	(FRAGMENT).									DE	BETA-SUBUNIT OF NITRILE HYDRATASE (FRAGMENT).
GN	CHRH-R.										OS	Rhodococcus sp.
OS	Homo sapiens (Human).										OC	Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;										OC	
OC	Eutheria; Primates; Catarrhini; Hominidae; Homo.										RN	[1]
RN	SEQUENCE FROM N.A.										RP	SEQUENCE FROM N.A.
RX	MEDLINE: 96001284.										RC	STRAIN=N-774;
RA	HASHIMOTO K., KOGA M., MOTOMURA T., KASAYAMA S., KOHARA H., OHNISHI T., ARITA N., HAYAKAWA T., SATO B., KISHIMOTO T.;										RX	MEDLINE; 95072315.
RA	"Identification of alternatively spliced messenger ribonucleic acid encoding truncated growth hormone-releasing hormone receptor in human pituitary adenomas".										RA	HASHIMOTO Y., NISHIYAMA M., HORINOUCHI S., BEPPU T.;
RT	J. Clin. Endocrinol. Metab. 80:2933-2939(1995).										RT	"Nitrile hydratase gene from Rhodococcus sp. N-774 requirement for its downstream region for efficient expression";
RT	EMBL: S79912; AAD143181; -.										RL	Biosci. Biotechnol. Biochem. 58:1659-1865(1994).
FT	NON-TER	1	1								DR	EMBL; D30033; BAA06273; 1; -.
SQ	SEQUENCE 13 AA:	1612 MW:	085914B2 CRC32;								DR	HSSP; P13449; 1AHJ.
Query Match	51.5%	Score 17;	DB 4;	Length 13;							FT	NON-TER
Best Local Similarity	66.%	Pred. No. 1.6e+03;									1	SEQUENCE 12 AA:
Matches	4;	Conservative /	0;	Mismatches /	2;	Indels	0;	Gaps	0;		1323 MW:	666FD346 CRC32;
Qy	2 GILERV 7										Query Match	48.5%;
Db	1										Best Local Similarity	60.0%;
Db	8 GYWERV 13										Matches	3; Conservative
RESULT	6										1;	Mismatches 1; Indels 0; Gaps 0;
Q77910											RESULT	8
ID	Q77910;										Q16007	PRELIMINARY;
AC	Q77910;										ID	Q16007;
DT	01-NOV-1998	(TREMBLrel.	08; Created)								AC	Q16007;
DT	01-NOV-1998	(TREMBLrel.	08; Last sequence update)								DT	01-NOV-1996 (TREMBLrel.
DT	01-NOV-1998	(TREMBLrel.	08; Last annotation update)								DT	01-NOV-1998 (TREMBLrel.
DE	MHC CLASS II B LOCUS 3 (FRAGMENT).										DE	LYSOSOMAL ACID BETA-GALACTOSIDASE (FRAGMENT).
OS	Oreochromis niloticus (Nilotic tilapia) (Tilapia nilotica).										OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii; Teleostei; Euteleoste;										OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
OC	Percomorphae; Labroidei; Cichlidae; Oreochromis.										OC	Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN	SEQUENCE FROM N.A.										RN	[1]
RX	MEDLINE: 98315113.										RP	SEQUENCE FROM N.A.
RA	MALAGA-TRILLO E., MCANDREW B., VINCEK V., ZALESKA-RUTCZYNKA Z., SUELTMANN H., FIGUEROA F., KUEIN J.;										RX	MEDLINE; 9136978.
RT	"Linkage relationships and haplotype polymorphism among cichlid Mhc class II B loci".										RA	MOREAU H., BONTEM E., ZHOU X.Y., D'AZZO A.;
RT	Genetics 149:1527-1547(1998).										RT	"Organization of the gene encoding human lysosomal beta-galactosidase";
RT	EMBL; AF050021; AAC11360; -.										RL	DNA Cell Biol. 10:495-504(1991).
KW	MHC.										DR	EMBL; S55584; AAB19814; -.
NON-TER	1	1									FT	NON-TER
FT	50.0%	Score 16;	DB 7;	Length 11;							13	SEQUENCE 13 AA:
SQ	SEQUENCE 11 AA:	1344 MW:	2E9158C4 CRC32;								1482 MW:	615C03BB CRC32;
Qy	2 GILERV 7										Qy	2 GILERV 7
Db	1										Db	3 GEYVR 8
RESULT	9										RESULT	Q97090

ID	Q97090; Q97090;	PRELIMINARY;	PRT;	15 AA.	
AC	DT 01-FEB-1997 (TREMBLrel. 02, Created)				
DT	01-FEB-1997 (TREMBLrel. 02, Last sequence update)				
DT	01-NOV-1998 (TREMBLrel. 08, Last annotation update)				
DE	GAG POLYPROTEIN (FRAGMENT).				
GN	GAG.				
OS	Human immunodeficiency virus type 1.				
OC	virusss; Retroviridae; Lentivirus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=LAI;				
RA	WEI Q., FUJITZ P.N.;				
RT	"Extensive diversification of human immunodeficiency virus type 1 subtype B strains during dual infection of a chimpanzee that progressed to AIDS";				
RT	J. Virol. 72:3005-3017(1998).				
RL	EMBL; U56889; AAC59299.1; -.				
KW	Polyprotein.				
FT	NON_TER 1 1				
SQ	SEQUENCE 15 AA; 1577 MW; 6B94DD64 CRC32;				
Query Match	Best Local Similarity 48.5%; Score 16; DB 12; Length 15;				
	Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;				
RESULT	10				
Q9X3M2	PRELIMINARY;	PRT;	10 AA.		
ID	Q9X3M2;				
AC	DT 01-NOV-1999 (TREMBLrel. 12, Created)				
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)				
DE	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
GN	CYTOKROME B (FRAGMENT).				
OS	Prochlorococcus sp.				
OC	Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae; Prochlorococcus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	URBACH E., CHISHOLM S.W.;				
RT	"Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";				
RT	LIMNO. Oceanog. 43:1615-1630(1998).				
RL	EMBL; AF070219; AAD3269.1; -.				
DR	NON_TER 1 1				
SQ	SEQUENCE 10 AA; 1076 MW; BCB27A24 CRC32;				
Query Match	Best Local Similarity 45.5%; Score 15; DB 2; Length 10;				
	Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
RESULT	11				
Q73594	PRELIMINARY;	PRT;	10 AA.		
ID	Q73594;				
AC	DT 01-AUG-1998 (TREMBLrel. 07, Created)				
DT	01-AUG-1998 (TREMBLrel. 07, Last sequence update)				
DE	01-NOV-1998 (TREMBLrel. 08, Last annotation update)				
DB	ZAX-2 (FRAGMENT).				
Query Match	Best Local Similarity 45.5%; Score 15; DB 2; Length 11;				
	Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;				
RESULT	12				
Q9X956	PRELIMINARY;	PRT;	11 AA.		
ID	Q9X956;				
AC	DT 01-NOV-1999 (TREMBLrel. 12, Created)				
DT	01-NOV-1999 (TREMBLrel. 12, Last sequence update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
OS	Streptomyces lividans.				
CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	STREPTOMYCETACEAE.				
GN	ORF9				
OS	Streptomyces lividans.				
CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
OS	Streptomyces lividans.				
CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
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OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
OS	Streptomyces lividans.				
CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
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GN	ORF9				
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OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
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OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
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OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
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GN	ORF9				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
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GN	ORF9				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
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GN	ORF9				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
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GN	ORF9				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
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GN	ORF9				
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OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
OS	Streptomyces lividans.				
CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
OS	Streptomyces lividans.				
CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
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GN	ORF9				
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OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
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OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
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GN	ORF9				
OS	Streptomyces lividans.				
CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
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GN	ORF9				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
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OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
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CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
OS	Streptomyces lividans.				
CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
OS	Streptomyces lividans.				
CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN	ORF9				
OS	Streptomyces lividans.				
CC	Bacteria; Firmicutes; Actinobacteridae;				
OC	Actinomycetales; Streptomyctaceae; Streptomyces.				
DT	01-NOV-1999 (TREMBLrel. 12, Last annotation update)				
DE	HYPOTHETICAL 1.2 KD PROTEIN (FRAGMENT).				
GN</					

OC	Neopterygia;	Teleostii;	Buteleosteii;	Acanthopterygii;	Percomorpha;
CC	Periformes;	Labroidei;	Cichlidae;	Oreochromis.	
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MALAGA-TRILLO E., MCANDREW B., VINCERK V., ZALESKA RUTCZYNSKA Z., SUELTMANN H., FIGUEROA F., KLEIN J.; "Linkage relationships and haplotype polymorphism among cichlid Mhc class II B loci." Genetics 149:1527-1547(1998).				
RA	MALETA-TRILLO E., FIGUEROA F., KLEIN J.; "Linkage relationships and haplotype polymorphism among cichlid Mhc class II B loci." Genetics 149:1527-1547(1998).				
DR	EMBL; AF050022; AAC1361.1; -.				
KW	MHC				
FT	NON_TER	1	1		
FT	NON_TER	11	11		
SQ	SEQUENCE	11 AA;	1401 MW;	FF3CCDF9 CRC32;	
Query Match	45.5%;	Score 15;	DB 7;	Length 11;	
Best Local Similarity	75.0%;	Pred. No. 3.e+03;			
Matches	3;	Conservative	0;	Mismatches 1;	Indels 0;
Gaps	0;				
Qy	2 GILE 5	PRELIMINARY;	PRT;	13 AA.	
Db	1 GFILE 4				
RESULT	14				
Q9X316	ID	Q9X3J6	PRELIMINARY;	PRT;	13 AA.
AC	Q9X3J6;				
DT	01-NOV-1999	(TREMBLrel. 12, Created)			
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)			
DT	01-NOV-1999	(TREMBLrel. 12, Last annotation update)			
DE	CYTOCHROME B (FRAGMENT).				
GN	PETB.				
OS	Prochlorococcus sp.				
OC	Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;				
OC	prochlorococcus.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	URBACH E., CHISHOLM S.W.; "Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso sea and Gulf Stream."; LIMNOLOG. OCEANOLOG. 43:1615-1630(1998).				
RL	EMBL; AF070189; AAD2225.1; -.				
FT	NON_TER	1	1		
SQ	SEQUENCE	13 AA;	1473 MW;	ECD3C1B2 CRC32;	
Query Match	45.5%;	Score 15;	DB 2;	Length 13;	
Best Local Similarity	100.0%;	Pred. No. 4.4e+03;			
Matches	3;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;				
Qy	1 QGI 3	PRELIMINARY;	PRT;	13 AA.	
Db	7 QGI 9				
RESULT	15				
Q9X3E1	ID	Q9X3E1	PRELIMINARY;	PRT;	13 AA.
AC	Q9X3E1;				
DT	01-NOV-1999	(TREMBLrel. 12, Created)			
DT	01-NOV-1999	(TREMBLrel. 12, Last sequence update)			
DT	01-NOV-1999	(TREMBLrel. 12, Last annotation update)			
DE	CYTOCHROME B (FRAGMENT).				
GN	PETB.				
OS	Prochlorococcus sp.				
OC	Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;				
OC	Prochlorococcus.				
RN	[1]				
RA	URBACH E., CHISHOLM S.W.;				
RP	SEQUENCE FROM N.A.				
RT	"Genetic diversity in Prochlorococcus populations flow cytometrically sorted from the Sargasso Sea and Gulf Stream.";				
RL	LIMNOLOG. OCEANOLOG. 43:1615-1630(1998).				
FT	NON_TER	1	1		
SQ	SEQUENCE	13 AA;	1473 MW;	ECD3C1B2 CRC32;	
Query Match	45.5%;	Score 15;	DB 2;	Length 13;	
Best Local Similarity	100.0%;	Pred. No. 4.4e+03;			
Matches	3;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;				
Qy	1 OGILVER 7	PRELIMINARY;	PRT;	15 AA.	
Db	5 KGFFHRI 11				
RESULT	17				
ID	Q9X3E1				
AC	Q9X3E1;				
DT	01-AUG-1998	(TREMBLrel. 07, Created)			
DT	01-AUG-1998	(TREMBLrel. 07, Last sequence update)			
DT	01-AUG-1998	(TREMBLrel. 07, Last annotation update)			
DE	TURGOR RESPONSIVE PROTEIN HOMOLOG (FRAGMENT).				
OS	Mesembryanthemum crystallinum (Common ice plant).				
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;				
OC	euphyllophytes; Spermatophyta; Magnoliophyta; eudicotyledons;				
OC	core eudicots; Caryophyllidae; Caryophyllales; Aizoaceae;				
OC	Mesembryanthemum.				
RN	SEQUENCE FROM N.A.				
RP	TISSUE-ROOT;				
RC	MICHAILOWSKI C.B., BOHNERT H.J.;				
RA	Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.				
RL	DR	Submitted (APR-1998) to the EMBL/GenBank/DBJ databases.			
EMBL; AF054444; AAC14178.1; -.					
FT	NON_TER	1	1		
SQ	SEQUENCE	15 AA;	1607 MW;	AD52368C CRC32;	

Query Match		Score 15;	DB 10;	Length 15;		Matches	3;	Conservative	2;	Mismatches	1;	Indels	0;	Gaps	0;
Best Local Similarity		100.0%	Pred. No. 5.1e+03;	Mismatches 0;	Indels 0;	Qy	1 QGTLER 6								
Matches	3;	Conservative				Db	10 RGDLDR 15								
Qy	1 QGTLER 6					RESULT 20									
Db	10 RGDLDR 15					010226	PRELIMINARY;								
						ID	010226;								
						AC	010226;								
						DT	01-JUL-1997 (TREMBLrel.	04,	Created)						
						DT	01-JUL-1997 (TREMBLrel.	04,	Last sequence update)						
						DT	01-MAY-1999 (TREMBLrel.	10,	Last annotation update)						
						DE	ENVLOPE GLYCOPROTEIN (FRAGMENT).								
						GN	ENV.								
						OS	Human immunodeficiency virus type 1.								
						OC	Viruses; Retroviridae; Lentivirus.								
						RN	[1]								
						RP	SEQUENCE FROM N.A.								
						RX	MEDLINE; 98216723.								
						RA	SALVI R., GARBIGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,								
						RA	BENEDETTO A.;								
						RT	"Grossly defective nef gene sequences in a human immunodeficiency								
						RT	virus type 1-seropositive long-term nonprogressor."								
						RL	J. Virol. 72:3646-3657(1998).								
						DR	EMBL; U89846; AAC26085.1; -.								
						DR	PFAM; PF00517; GP41. 1.								
						KW	Envelope Protein.								
						FT	NON-TER	1	1	1	1	1	1	1	
						SQ	SEQUENCE 14 AA; 1691 MW; C5EBD4F9 CRC32;								
						Query Match	Score 43.9%;	Score 43.45%;	Score 43.9%;	Score 43.45%;	Score 43.9%;	Score 43.45%;	Score 43.9%;	Score 43.45%;	
						Best Local Similarity	83.38;	83.38;	83.38;	83.38;	83.38;	83.38;	83.38;	83.38;	
						Matches	5;	Conservative	0;	Mismatches	0;	Indels	1;	Gaps	1;
						Qy	1 QGTLER 6								
						Db	7 QG-LER 11								
						RESULT 21									
						010227	PRELIMINARY;								
						ID	010227;								
						AC	010227;								
						DT	01-JUL-1997 (TREMBLrel.	04,	Created)						
						DT	01-JUL-1997 (TREMBLrel.	04,	Last sequence update)						
						DT	01-MAY-1999 (TREMBLrel.	10,	Last annotation update)						
						DE	ENVLOPE GLYCOPROTEIN (FRAGMENT).								
						GN	ENV.								
						OS	Human immunodeficiency virus type 1.								
						OC	Viruses; Retroviridae; Lentivirus.								
						RN	[1]								
						RP	SEQUENCE FROM N.A.								
						RX	MEDLINE; 98216723.								
						RA	SALVI R., GARBIGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,								
						RA	BENEDETTO A.;								
						RT	"Grossly defective nef gene sequences in a human immunodeficiency								
						RT	virus type 1-seropositive long-term nonprogressor."								
						RL	J. Virol. 72:3646-3657(1998).								
						DR	EMBL; U89847; AAC26086.1; -.								
						DR	PFAM; PF00517; GP41. 1.								
						KW	Envelope Protein.								
						FT	NON-TER	1	1	1	1	1	1	1	
						SQ	SEQUENCE 14 AA; 1691 MW; C5EBD4F9 CRC32;								
						Query Match	Score 43.9%;	Score 43.45%;	Score 43.9%;	Score 43.45%;	Score 43.9%;	Score 43.45%;	Score 43.9%;	Score 43.45%;	
						Best Local Similarity	83.38;	83.38;	83.38;	83.38;	83.38;	83.38;	83.38;	83.38;	
						Matches	5;	Conservative	0;	Mismatches	0;	Indels	1;	Gaps	1;
						Qy	1 QGTLER 6								

Db 7 QG-LER 11

RESULT 22
 ID O10228 PRELIMINARY; PRT; 14 AA.
 AC 010228; 1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98216723.
 RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,
 RA BENDETTI A.;
 RT "Grossly defective nef gene sequences in a human immunodeficiency
 virus type 1-seropositive long-term nonprogressor.";
 RT Virus type 1-seropositive long-term nonprogressor.;
 RL J. Virol. 72:3646-3657(1998).
 EMBL; U89848; AAC26087.1; -.
 PFAM; PF00517; GP41; 1.
 DR Envelope protein.
 FT NON-TER 1
 SQ SEQUENCE 14 AA; 1691 MW; DF06B562 CRC32;

Query Match Score 43.9%; Pred. No. 6.1e+03; Length 14;
 Best Local Similarity 83.3%;保守性 Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 OGILVER 6
 Db 7 QG-LER 11

RESULT 23
 ID O10229 PRELIMINARY; PRT; 14 AA.
 AC 010229; 1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98216723.
 RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,
 RA BENDETTI A.;
 RT "Grossly defective nef gene sequences in a human immunodeficiency
 virus type 1-seropositive long-term nonprogressor.";
 RL J. Virol. 72:3646-3657(1998).
 EMBL; U89852; AAC26091.1; -.
 PFAM; PF00517; GP41; 1.
 DR Envelope protein.
 FT NON-TER 1
 SQ SEQUENCE 14 AA; 1721 MW; C5EBD4F9 CRC32;

Query Match Score 43.9%; Pred. No. 6.1e+03; Length 14;
 Best Local Similarity 83.3%;保守性 Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 OGILVER 6
 Db 7 QG-LER 11

RESULT 24
 ID O10230 PRELIMINARY; PRT; 14 AA.
 AC 010230; 1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98216723.
 RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,
 RA BENDETTI A.;
 RT "Grossly defective nef gene sequences in a human immunodeficiency
 virus type 1-seropositive long-term nonprogressor.";
 RL J. Virol. 72:3646-3657(1998).
 EMBL; U89850; AAC26089.1; -.
 PFAM; PF00517; GP41; 1.
 DR Envelope protein.
 FT NON-TER 1
 SQ SEQUENCE 14 AA; 1721 MW; DF06B562 CRC32;

Query Match Score 43.9%; Pred. No. 6.1e+03; Length 14;
 Best Local Similarity 83.3%;保守性 Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 OGILVER 6
 Db 7 QG-LER 11

RESULT 25
 ID O10232 PRELIMINARY; PRT; 14 AA.
 AC 010232; 1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-1999 (TREMBLrel. 10, Last annotation update)
 DE ENVELOPE GLYCOPROTEIN (FRAGMENT).
 ENV.
 OS Human immunodeficiency virus type 1.
 OC Viruses; Retroviridae; Lentivirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 98216723.
 RA SALVI R., GARBUGLIA A.R., DI CARO A., PULCIANI S., MONTELLA F.,
 RA BENDETTI A.;
 RT "Grossly defective nef gene sequences in a human immunodeficiency
 virus type 1-seropositive long-term nonprogressor.";
 RL J. Virol. 72:3646-3657(1998).
 EMBL; U89852; AAC26091.1; -.
 PFAM; PF00517; GP41; 1.
 DR Envelope protein.
 FT NON-TER 1
 SQ SEQUENCE 14 AA; 1691 MW; C5EBD4F9 CRC32;

Query Match Score 43.9%; Pred. No. 6.1e+03; Length 14;
 Best Local Similarity 83.3%;保守性 Matches 5; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 OGILVER 6
 Db 7 QG-LER 11

RESULT 26
 ID O10233

OC Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE OF 90-98 FROM N.A.
RX MEDLINE; 88234523.
RA KAWAKAMI T., KAWAKAMI Y., AARONSON S.A., ROBBINS K.C.;
RT "Acquisition of transforming properties by FYN, a normal SRC-related
human gene.";
RR Proc. Natl. Acad. Sci. U.S.A. 85:3870-3874 (1988).
RL EMBL: M20284; AAA52491.1; -.
DR EMBL: M20284; AAA52491.1; -.
FT NON_TER 1 1 MW:
SEQUENCE 9 AA: 1143 MW: C710793C CRC32;

Query Match 42.4%; Score 14; DB 4; Length 9;
Best Local Similarity 60.0%; Pred. No. 2.3e+05;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 OGILE 5
 | |
 D 4 QSFILE 8

Search completed: June 30, 2000, 16:18:47
Job time: 7898 sec

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KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis.
 OS Homo sapiens.

FH Key Location/Qualifiers

FT Modified_site 12
 /note= "Asn residue amidated"

FT WO945710-A1.
 PD 15-OCT-1998.
 PR 11-APR-1997; U06500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/WEBBER R.
 PI Webber R;
 DR WPI; 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunosassay in which a sample is contacted with a specific binding
 entity reactive with human iNOS or mimics.
 PS Example 4: Page 36; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 specific binding entity (e.g. a monoclonal antibody) reactive to human
 inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 to detect the presence of human iNOS protein in the sample. The method
 can be used for the detection and quantitation of human iNOS in cells and
 tissues for various pathophysiological conditions such as sepsis, septic
 shock, myocardial infarction, rejection of tissue in organs following
 transplantation, monitoring "flare ups" in certain autoimmune diseases
 such as lupus, psoriasis, and multiple sclerosis. This sequence
 represents a peptide from human iNOS which is used in the method of the
 CC invention.
 CC invention. 12 AA;

Query Match 100.0%; Score 35; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTQDDLQ 7
 ID W81268 standard; peptide; 12 AA.
 AC W81268;
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment PS-5266.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis.
 OS Homo sapiens.

RESULT 6
 ID W81268
 ID W81268 standard; peptide; 12 AA.
 AC W81268;
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment PS-5266.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis.
 OS Homo sapiens.

Location/Qualifiers

FT Modified_site 15
 FT WO945710-A1.
 PT /note= "Lys residue amidated"
 PD 15-OCT-1998.
 PR 07-APR-1997; U06500.
 PA (WEBB/WEBBER R.
 PI Webber R;
 DR WPI; 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunosassay in which a sample is contacted with a specific binding
 entity reactive with human iNOS or mimics.
 PS Example 12; Page 54; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 specific binding entity (e.g. a monoclonal antibody) reactive to human
 inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 to detect the presence of human iNOS protein in the sample. The method
 can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathophysiological conditions such as sepsis, septic
 shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the
 CC invention.
 Sequence 12 AA;

Query Match 100.0%; Score 35; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 0.1;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTQDDLQ 7
 ID W81293 standard; peptide; 12 AA.
 AC W81293;
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment #14.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis; epitope mapping.
 OS Homo sapiens.
 PN WO945710-A1.
 PD 15-OCT-1998.
 PR 11-APR-1997; U06500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/WEBBER R.
 PI Webber R;
 DR WPI; 98-594495/50.
 PT Detection of human inducible nitric oxide synthase - using an
 PT immunosassay in which a sample is contacted with a specific binding
 entity reactive with human iNOS or mimics.
 PS Example 4; Fig 7B; 93pp; English.
 CC This invention describes an immunoassay method where a sample with a
 specific binding entity (e.g. a monoclonal antibody) reactive to human
 inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 to detect the presence of human iNOS protein in the sample. The method
 can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathophysiological conditions such as sepsis, septic
 shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the

Location/Qualifiers

RESULT 7
 ID W81227
 ID W81227 standard; peptide; 15 AA.
 AC W81227;
 DT 30-APR-1999 (first entry)
 DE Human iNOS peptide fragment PS-5265.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis.
 OS Homo sapiens.

Location/Qualifiers

FT	Modified_site	15	<i>/note- "Lys residue amidated"</i>									
PN	W0945710-A1.											
PD	15-OCT-1998.											
PP	11-APR-1997; U06500.											
PR	07-APR-1997; US-667777.											
PA	(WEBB/)	WEBBER R.										
PI	Webber R.											
DR	WPI; 98-594495/50.											
PT	Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.											
PS	Example 4: Page 36; 93pp; English.											
CC	This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the invention.											
SQ	Sequence 15 AA;											
FT	Modified_site	15										
PN	W0945710-A1.											
PD	15-OCT-1998.											
PP	11-APR-1997; U06500.											
PR	07-APR-1997; US-667777.											
PA	(WEBB/)	WEBBER R.										
PI	Webber R.											
DR	WPI; 98-594495/50.											
PT	Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.											
PS	This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the invention.											
CC	Sequence 15 AA;											
FT	Modified_site	15										
PN	W0945710-A1.											
PD	15-OCT-1998.											
PP	11-APR-1997; U06500.											
PR	07-APR-1997; US-667777.											
PA	(WEBB/)	WEBBER R.										
PI	Webber R.											
DR	WPI; 98-594495/50.											
PT	Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.											
PS	Example 4: Fig 7B; 93pp; English.											
CC	This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the invention.											
SQ	Sequence 15 AA;											
FT	Modified_site	15										
PN	W0945710-A1.											
PD	15-OCT-1998.											
PP	11-APR-1997; U06500.											
PR	07-APR-1997; US-667777.											
PA	(WEBB/)	WEBBER R.										
PI	Webber R.											
DR	WPI; 98-594495/50.											
PT	Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.											
PS	Example 4: Fig 7B; 93pp; English.											
CC	This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the invention.											
SQ	Sequence 15 AA;											
FT	Modified_site	15										
PN	W0945710-A1.											
PD	15-OCT-1998.											
PP	11-APR-1997; U06500.											
PR	07-APR-1997; US-667777.											
PA	(WEBB/)	WEBBER R.										
PI	Webber R.											
DR	WPI; 98-594495/50.											
PT	Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.											
PS	Example 4: Fig 7B; 93pp; English.											
CC	This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the invention.											
SQ	Sequence 15 AA;											
FT	Modified_site	15										
PN	W0945710-A1.											
PD	15-OCT-1998.											
PP	11-APR-1997; U06500.											
PR	07-APR-1997; US-667777.											
PA	(WEBB/)	WEBBER R.										
PI	Webber R.											
DR	WPI; 98-594495/50.											
PT	Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.											
PS	Example 4: Fig 7B; 93pp; English.											
CC	This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the invention.											
SQ	Sequence 15 AA;											
FT	Modified_site	15										
PN	W0945710-A1.											
PD	15-OCT-1998.											
PP	11-APR-1997; U06500.											
PR	07-APR-1997; US-667777.											
PA	(WEBB/)	WEBBER R.										
PI	Webber R.											
DR	WPI; 98-594495/50.											
PT	Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.											
PS	Example 4: Fig 7B; 93pp; English.											
CC	This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the invention.											
SQ	Sequence 15 AA;											
FT	Modified_site	15										
PN	W0945710-A1.											
PD	15-OCT-1998.											

PR	07-APR-1997; US-667777.	Db	1 TQDDLQ 6
PA	(WEBB/) WEBBER R.		
PI	Webber R.		
DR	WPI: 98-594495/50.		
PR	Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.		
PR	Example 4; Page 35; 93PP; English.		
CC	This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody), reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the invention. Sequence 15 AA.		
SQ			
Query Match	88.6%; Score 31; DB 1; Length 15;	RESULT 12	
Best Local Similarity	100.0%; Pred. No. 0.89;	ID	W81265 standard; peptide; 9 AA.
Matches	0; Mismatches 0; Indels 0; Gaps 0;	AC	W81265;
Qy	2 TQDDLQ 7	DT	30-APR-1999 (first entry)
Db	1 TQDDLQ 6	DE	Human iNOS peptide fragment PS-5236.
RESULT 11		KW	Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
WD	W81288 standard; peptide; 15 AA.	CC	monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
AC	W81288;	DE	myocardial infarction; tissue rejection; transplantation; psoriasis;
PR	07-APR-1999 (first entry)	KW	autoimmune disease; multiple sclerosis.
PA	Human iNOS peptide fragment mapping #9.	OS	Homo sapiens.
PI	Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;	Key	
DR	monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;	Modified_site	10
PR	myocardial infarction; tissue rejection; transplantation; psoriasis;	/note=	"Leu residue amidated"
PT	autoimmune disease; multiple sclerosis; epitope mapping.		
OS	W09845710-A1.		
PN	15-OCT-1998.	Query Match	85.7%; Score 30; DB 1; Length 9;
PF	07-APR-1997; US-667777.	Best Local Similarity	100.0%; Pred. No. 1.5e+05;
PA	(WEBB/) WEBBER R.	Matches	0; Mismatches 0; Indels 0; Gaps 0;
PI	Webber R.	Qy	1 VTQDDL 6
DR	WPI: 98-594495/50.	Db	4 VTQDDL 9
PT	Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.	RESULT 13	
PS	Example 4; Fig 7A; 93PP; English.	ID	W81270 standard; peptide; 10 AA.
CC	This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody), reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the invention. Sequence 15 AA.	AC	W81270;
SQ		DT	30-APR-1999 (first entry)
Query Match	88.6%; Score 31; DB 1; Length 15;	DE	Human iNOS peptide fragment PS-5269.
Best Local Similarity	100.0%; Pred. No. 0.89;	KW	Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
Matches	0; Mismatches 0; Indels 0; Gaps 0;	CC	monoclonal antibody; mimic; quantitation; sepsis; septic shock; lupus;
Qy	2 TQDDLQ 7	DE	myocardial infarction; tissue rejection; transplantation; psoriasis;
Db	1 TQDDLQ 6	KW	autoimmune disease; multiple sclerosis.
RESULT 14		OS	Homo sapiens.
WD	W09845710-A1.	Key	
AC	15-OCT-1998.	Modified_site	10
PR	07-APR-1997; US-667777.	/note=	"Leu residue amidated"
PA	(WEBB/) WEBBER R.		
PI	Webber R.		
DR	WPI: 98-594495/50.		
PT	Detection of human inducible nitric oxide synthase - using an immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.		

PT immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
 PT Example 12; Page 54; 93pp; English.
 PS This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the invention. Sequence 10 AA;

Query Match 85.7%; Score 30; DB 1; Length 10;
 Best Local Similarity 100.0%; Pred. No. 0.91;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 VTQDDL 6
 Db 5 VTQDDL 10

RESULT 14
 W81266 ID W81266 standard: peptide; 9 AA.
 AC W81266;
 DT 30-APR-1999 (first entry)
 Human iNOS peptide fragment PS-5257.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection; monoclonal antibody; mimic; quantitation; sepsis; shock; lupus;
 myocardial infarction; tissue rejection; transplantation; psoriasis;
 autoimmune disease; multiple sclerosis.
 OS Homo sapiens. Location/Qualifiers
 FT Modified site 9 FT
 /note= "Asp residue amidated"
 PN W09845710-A1.
 PD 15-OCT-1998.
 PF 11-APR-1997; 006500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PI Webber R;
 DR WPI: 98-594495/50.
 PT immunoassay in which a sample is contacted with a specific binding entity reactive with human iNOS or mimics.
 PS Example 12; Page 55; 93pp; English.
 This invention describes an immunoassay method where a sample with a specific binding entity (e.g. a monoclonal antibody) reactive to human inducible nitric oxide synthase (iNOS) or mimics of this Protein is used to detect the presence of human iNOS protein in the sample. The method can be used for the detection and quantitation of human iNOS in cells and tissues for various pathophysiological conditions such as sepsis, septic shock, myocardial infarction, rejection of tissue in organs following transplantation, monitoring "flare ups" in certain autoimmune diseases such as lupus, psoriasis, and multiple sclerosis. This sequence represents a peptide from human iNOS which is used in the method of the invention. Sequence 9 AA;

Query Match 74.3%; Score 26; DB 1; Length 9;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05; Mismatches 5; Indels 0; Gaps 0;
 Qy 1 VTQDD 5
 Db 5 VTQDD 9

RESULT 15
 ID R20282 standard: peptide; 15 AA.
 AC R20282;
 DT 26-DEC-1991 (first entry)
 Beta-2 integrin peptide derived from CD11b alpha subunit.
 KW Immune response; phagocyte-mediated tissue damage; A domain; MAM; complement receptor type 3; heterodimer; CR3; Mol; Mav-1; Synthetic.
 OS WO919511-A.
 PN 26-DEC-1991.
 PD 18-JUN-1991; U04338.
 PF 18-JUN-1990; US-539842.
 PR 04-JAN-1991; US-637830.
 PA (GEMO) GEN HOSPITAL CORP.
 PI Arnaout MA;
 DR WPI: 92-024197/03.
 Beta-2 integrin Peptide CD11b, recombinant hetero-dimer CD11b/CD18 or MAB against them; useful for inhibiting CD11b/CD18 mediated immune response in control of phagocyte-mediated tissue damage.
 PT
 PS Claim 8; Page 73; 84pp; English.
 The peptide (SEQ ID NO: 29) corresponds to residues 750-764 of CD11b alpha subunit of beta 2 integrin. The peptide may be synthesised or prep. by recombinant techniques using the gene, the sequence of which was disclosed by Arnalot et al., J. Cell Biol. 106:2153 (1988).
 CC (References are also provided for the DNA sequences of human CD18, CC CD11b and CD11a). The peptide is capable of inhibiting a CD11b/CD18 mediated immune response and is useful for treatment of ischaemia reperfusion injury, burns, frostbite, acute arthritis, asthma and adult respiratory distress syndrome. It may also be used to block CC intra-islet infiltration of macrophages associated with insulin-dependent diabetes mellitus, and for controlling phagocyte-mediated tissue damage to heart muscle during acute cardiac insufficiency.
 CC See also R20256-R20299.
 SQ Sequence 15 AA;

Query Match	65.7%	Score 23;	DB 1;	Length 15;
Best Local Similarity	66.7%	Pred. No. 43;	Mismatches 1;	
Matches	4;	Conservative	Indels 0;	Gaps 0;

Qy 1 VTQDDL 6
 DR 1 : |||||
 Db 10 ICQDDL 15

RESULT 16
 ID W02070 standard: peptide; 15 AA.
 AC W02070;
 DT 09-APR-1997 (first entry)
 Human beta 2 integrin subunit CD11b, residues 750-764.
 DE Beta 2 integrin; A domain; metal binding domain; inflammatory response; KW immune response; inhibition; phagocyte-mediated tissue injury; KW inflammation.
 OS Homo sapiens.
 PN WO9624063-A1.
 PD 08-AUG-1996.
 PR 30-JAN-1995; U01314.
 PA (GEMO) GEN HOSPITAL CORP.
 PI Arnaout MA;
 DR WPI: 96-371576/37.
 PT In vitro identification of integrin function antagonists - by measuring binding of A-domain peptide derived from integrin to ligand in presence and absence of candidate antagonist.
 PT Disclosure; Page 11; 111pp; English.
 PS The sequences given in W02037-80 represent peptides derived from beta2 integrin, esp. A-domain and the metal binding domains. These CC

CC peptides were selected using the method of the invention which
 CC screens compounds for their ability to inhibit the binding of a
 CC selected integrin to a ligand which naturally binds to it. The
 CC method comprises measuring the binding of an A-domain peptide
 CC derived from the selected integrin, to the ligand in the presence
 CC and absence of the test compound and determining whether the binding
 CC is decreased. Identified compounds are capable of interfering with
 CC certain cellular immune/inflammatory responses, particularly
 CC phagocyte-mediated tissue injury and inflammation. The numbering
 CC of the amino acid residues is based on the deduced amino acid
 CC sequence of the open reading frame of human CD11b from Arnaout et al.,
 CC J. Cell. Biol. 106:2153 (1988).
 SQ Sequence 15 AA; 15 AA;

Query Match 65.7%; Score 23; DB 1; Length 15;
 Best Local Similarity 66.7%; Pred. No. 43;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 VQDDL 6
 Db 10 IQQDL 15

RESULT 17
 W53913 standard; Peptide: 8 AA.
 ID W53913
 AC W53913
 DR 17-AUG-1998 (first entry)
 DE Interleukin-1 receptor accessory molecule epitope K320-K327.
 KW Interleukin-1 receptor accessory molecule; IL-1R AcM; human;
 KW signal transduction; agonist; antagonist; antibody; infection;
 KW septic shock; inflammation; rheumatoid arthritis; therapy; epitope;
 KW antigen.
 OS Homo sapiens.
 PN W0980869-A1.
 PD 05-MAR-1998.
 PR 26-AUG-1996; WO-013954.
 PA (HOMA-) HUMAN GENOME SCI INC.
 PI Bednark DP, Olsen HS, Rossen CA;
 DR WPI; 98-230267/20.
 PR Nucleic acid encoding interleukin-1 receptor accessory protein -
 PR used for therapeutic modulation of IL-1 activity
 PS Claim 17; Page 83; 95bp; English.
 CC This peptide corresponds to amino acids 320-327 of novel human
 CC interleukin-1 receptor accessory molecule (IL-1R AcM) (see W53897),
 CC a new member of the immunoglobulin superfamily that forms a complex
 CC with type 1 IL-1R. It comprises an epitope-bearing portion of
 CC IL-1R AcM. 18 Antigenic peptides comprising epitope-bearing
 CC portions of human IL-1R AcM are claimed (see W53898-915). These
 CC can be used to generate soluble IL-1R AcM-specific antibodies,
 CC and may be produced by chemical synthesis or by recombinant means
 CC using nucleic acid molecules (see V2659) of the invention. The
 CC antibodies are useful as immunoassay reagents for detecting
 CC IL-1R AcM, for affinity purification of IL-1R AcM and for
 CC identifying cells that express IL-1R AcM.
 SQ Sequence 8 AA;

Query Match 62.9%; Score 22; DB 1; Length 8;
 Best Local Similarity 57.1%; Pred. No. 1.5e+05; Length 8;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 1 VTTDDLQ 7
 Db 2 VTSSEDLK 8

RESULT 18
 W5486 standard; Peptide: 12 AA.
 AC W35486;
 DR 16-OCT-1997; D00146.
 PR 03-APR-1997; DK-000398.
 PA (PPR-) PEPPERSEARCH AS.
 PI Heegaard PMH, Jakobsen PH;
 DR W97-512645/47.
 PR Non-dendritic peptide carrier linked to a solid phase - useful as a
 PT diagnostic agent and as a scaffold for production of chemical
 PS derivatives
 Example 7; Page 99; 262pp; English.
 CC A non-dendritic peptide carrier (A) has been developed which is coupled
 CC through a linker to a solid phase, forming a complex of (A)-solid phase.
 CC Where (A) comprises 10-50 amino acids capable of forming a secondary
 CC structure in a benign buffer after liberation from the solid phase, and

DT 22-APR-1998 (first entry)
 DE Proteoglycan associated lipoprotein Peptide 1.
 KW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
 KW scaffold; inhibition; metastasis;
 OS Actinobacillus pleuropneumoniae.
 PN WO9738011-A1.
 PD 16-OCT-1997.
 PR 03-APR-1996; DK-000398.
 PA (PPR-) PEPPERSEARCH AS.
 PI Heegaard PMH, Jakobsen PH;
 DR WPI; 97-512645/47.
 PR Non-dendritic peptide carrier linked to a solid phase - useful as a
 PT diagnostic agent and as a scaffold for production of chemical
 PT derivatives
 PS Example 5; Page 89; 262pp; English.
 CC A non-dendritic peptide carrier (A) has been developed which is coupled
 CC through a linker to a solid phase forming a complex of (A)-solid phase.
 CC Where (A) comprises 10-50 amino acids capable of forming a secondary
 CC structure in a benign buffer after liberation from the solid phase, and
 CC further the (A)-solid phase complex comprises an immunogenic substance
 CC and/or an immune mediator coupled on (A). The present sequence
 CC represents a peptide used in an example from the present invention. An
 CC chemical derivatives, characterised by covalently attaching molecules at
 CC attachment points. Alternatively (A) is used as a scaffold for the production of
 CC the incorporation into an Immunostimulating Complex (Iscom) resulting in
 CC (A)-Iscom complex which is used for the chemical coupling of antigenic
 CC substances in an aqueous solution by conjugation. (A) derivatised with
 CC one or more peptides having fibronectin-laminin- or vitronectin-like
 CC binding activities can be used for the promotion of cell-attachment to
 CC plastic surfaces, in particular to inhibit tumour growth and metastasis,
 CC and for promotion of wound healing. Also a derivatised (A) can be used
 CC for the selection of specifically-binding aptamers or as a diagnostic
 CC agent. Such diagnostic (A) molecules could be used to detect molecules
 CC derived from or indicative of pregnancy or of a disease, such as an
 CC infectious, autoimmune or cancerous disease.
 SQ Sequence 12 AA;

Query Match 62.9%; Score 22; DB 1; Length 12;
 Best Local Similarity 57.1%; Pred. No. 54;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VTTDDLQ 7
 Db 2 MTAEDLQ 8

RESULT 19
 W35498 standard; Peptide: 13 AA.
 ID W53498
 AC W35498;
 DR 22-APR-1998 (first entry)
 DE Pal A peptide from WO9738011.
 KW T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour;
 KW scaffold; inhibition; metastasis; wound healing; solid phase.
 OS Unidentified.
 PN WO9738011-A1.
 PD 16-OCT-1997.
 PR 03-APR-1997; D00146.
 PA (PPR-) PEPPERSEARCH AS.
 PI Heegaard PMH, Jakobsen PH;
 DR W97-512645/47.
 PR Non-dendritic peptide carrier linked to a solid phase - useful as a
 PT diagnostic agent and as a scaffold for production of chemical
 PS derivatives
 Example 7; Page 99; 262pp; English.
 CC A non-dendritic peptide carrier (A) has been developed which is coupled
 CC through a linker to a solid phase, forming a complex of (A)-solid phase.
 CC Where (A) comprises 10-50 amino acids capable of forming a secondary
 CC structure in a benign buffer after liberation from the solid phase, and

further the (A)-solid phase complex comprises an immunogenic substance and/or an immune mediator coupled on '(A)'. The present sequence represents a peptide used in an example from the present invention. An (A)-solid phase complex can be used as a scaffold for the production of chemical derivatives, characterised by covalently attaching molecules at attachment points. Alternatively '(A)' is used as a scaffold peptide for the incorporation into an Immunostimulating Complex ('Iscon') resulting an (A)-Iscon complex which is used for the chemical coupling of antigenic substances in an aqueous solution by conjugation. '(A)' derivatised with one or more peptides having fibronectin-, laminin- or vitronectin-like binding activities can be used for the promotion of cell-attachment to plastic surfaces, in particular to inhibit tumour growth and metastasis, and for promotion of wound healing. Also a derivatised '(A)' can be used for the selection of specifically-binding aptamers or as a diagnostic agent. Such diagnostic '(A)' molecules could be used to detect molecules derived from or indicative of pregnancy or of a disease, such as an infections, autoimmune or cancerous disease.

Sequence 13 AA;

Query Match 62.9%; Score 22; DB 1; Length 13;
Best Local Similarity 57.1%; Pred. No. 59;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VTTDDLQ 7
Db 3 MTADDLQ 9

RESULT 20

W12358 ID W12358 standard; protein; 14 AA.
AC W12358 (first entry)
DT 13-NOV-1997 DE Human hsp60 Peptide p39 (343-366);
KW Heat-shock protein; hsp; hsp60; insulin-dependent diabetes mellitus;
KW IDDM; OS Homo sapiens.
PN W09701959-A1.

PD 23-JAN-1997.

PF 01-JUL-1996; 011375.

PR 30-JUN-1995; IL-114407.

PA (YEDA RES & DEV CO LTD.

PI Abulafia R, Bockova J, Cohen IR, Elias D;

DR WPI: 97-108693/10

PT New peptide(s), derived from human heat-shock protein 60 - used for early diagnosis, prevention and treatment of insulin-dependent diabetes mellitus.

Claim 1; Page 13; 49PP; English.

The peptides given in W12346 to W12358 are derived from human hsp60 (W12345) and are useful for early diagnosis of IDDM by detecting, in the blood or urine, antibodies or T cells immunologically reactive with human hsp60 (presence of which indicates high probability of diabetes or its subsequent development). Other peptides (W12359 to W12361) were shown not to be as effective.

Sequence 14 AA;

Query Match 62.9%; Score 22; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 65;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTTDD 5
Db 8 VTRDD 12

RESULT 21
W33050 ID W33050 standard; peptide; 14 AA.
AC W33050 (first entry)
DT 26-JAN-1998

PR 14-MAY-1991; WO-003346.

PA (SHASHOUA VE.

PI Shashoua VE;

DR WPI: 92-41545/50.

PT Protein fragment comprising neuro-active domain of ependymin - enhances nerve connectivity and growth and is for treating nervous system disorders e.g. Huntington's, Parkinson's, and Alzheimer's diseases

PT Claim 21; Page 53; 77PP; English.

CC The fragment is that of an active region of the ependymin neuroactive domain (gamma chain amino acids 164-169) effective in stimulating nerve growth and elongation. It is 85.7% homologous to epidermal growth factor amino acids 169-175. It can be used to treat nerve injuries and to correct genetic or systemic disorders, e.g. treatment of Huntington's, Parkinson's or Alzheimer's diseases, or to pretreat nerve tissue before transplantation. It can be administered in sustained release form and may be coupled to a carrier which protects it against decomposition in the stomach and blood stream after oral admin. and carries it across the blood brain barrier, opt. with subsequent release of the free fragment in the brain.

CC Sequence 6 AA;

DE Human heat shock protein 60 residues 343-366.
KW Treatment; T cell mediated; disease; condition; antigen; human;
KW inflammatory T cell; pathogenesis; heat shock protein 60; hsp60;
KW insulin dependent diabetes mellitus; IDDM.
CC Home sapiens
OS
PN W09702016-A1.
PD 23-JAN-1997.
PF 02-JUL-1996; 011373.
PR 05-JUL-1995; IL-114458.
PA (YEDA RES & DEV CO LTD.
PI Cohen IR, Elias D, Shinitzky M;
DR WPI: 97-108732/10.
PT Prepn. for treatment of T cell mediated diseases such as diabetes or multiple sclerosis - comprises antigen recognised by inflammatory T cells, and a fat emulsion carrier comprising e.g. soybean oil, egg phospholipid and glycerol.
PT Disclosure; Page 6; 39pp; English.
CC A preparation for the treatment of T cell mediated diseases or conditions, comprises a carrier, comprising 10-20% triglycerides and 1-2-2.4% phospholipids of plant and/or animal origin, 2.25-4.5% osmo-regulator, 0-0.05% antioxidant and sterile water (to 100 ml), and an antigen recognised by inflammatory T cells associated with the pathogenesis of the disease or condition. The preparation can be used to treat insulin dependent diabetes mellitus, when the antigen is a peptide derived from heat shock protein 60 (e.g. the present peptide). The emulsions promote a TH1 to TH2 cytokine shift.
SQ Sequence 14 AA;

Query Match 62.9%; Score 22; DB 1; Length 14;
Best Local Similarity 80.0%; Pred. No. 65;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTTDD 5
Db 8 VTRDD 12

RESULT 22
R29290 ID R29290 standard; peptide; 6 AA.
AC R29290;
DT 07-APR-1993 (first entry)
DE Nerve growth stimulating protein fragment.
KW Ependymin; neuroactive domain; treatment; Huntington's chorea; Parkinson's disease; Alzheimer's disease.
OS Synthetic.
PN W020362-A.
PD 26-NOV-1992.
PF 14-MAY-1991; WO3346.
PR 14-MAY-1991; WO-003346.
PA (SHASHOUA VE.

PI Shashoua VE;

DR WPI: 92-41545/50.

PT Protein fragment comprising neuro-active domain of ependymin - enhances nerve connectivity and growth and is for treating nervous system disorders e.g. Huntington's, Parkinson's, and Alzheimer's diseases

PT Claim 21; Page 53; 77PP; English.

CC The fragment is that of an active region of the ependymin neuroactive domain (gamma chain amino acids 164-169) effective in stimulating nerve growth and elongation. It is 85.7% homologous to epidermal growth factor amino acids 169-175. It can be used to treat nerve injuries and to correct genetic or systemic disorders, e.g. treatment of Huntington's, Parkinson's or Alzheimer's diseases, or to pretreat nerve tissue before transplantation. It can be administered in sustained release form and may be coupled to a carrier which protects it against decomposition in the stomach and blood stream after oral admin. and carries it across the blood brain barrier, opt. with subsequent release of the free fragment in the brain.

CC Sequence 6 AA;

PA (WEBB/) WEBBER R.
 PT Webber R;
 DR WPI: 98-594495/50.
 PR Detection of human inducible nitric oxide synthase - using an
 PR immunoassay in which a sample is contacted with a specific binding
 PR entity reactive with human iNOS or mimics.
 PS Example 4; Page 34; 93PP; English.
 CC This invention describes an immunoassay method where a sample with a
 CC specific binding entity (e.g., a monoclonal antibody) reactive to human
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 CC to detect the presence of human iNOS protein in the sample. The method
 CC can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathophysiological conditions such as sepsis, septic
 CC shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the
 CC invention.
 SQ Sequence 6 AA:

Query Match 57.1%; Score 20; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQD 4
 |||||
 DB 3 VTQD 6

RESULT 30

WB1230 WB1230 standard; peptide: 6 AA.
 AC W81230;
 ID W81230; 30-APR-1999 (first entry)
 DE Human iNOS Peptide fragment PS-5268.
 KW Inducible; nitric oxide synthase; iNOS; human; immunoassay; detection;
 KW monoclonal antibody; mimic; quantitation; sepsis; shock; lupus;
 KW myocardial infarction; tissue rejection; transplantation; psoriasis;
 KW autoimmune disease; multiple sclerosis.
 OS Homo sapiens.
 EH Location/Qualifiers
 FT Modified_site 6
 FT /note= "Asp residue amidated"
 PN W09845710-A1.

PD 15-OCT-1998.
 PF 11-APR-1997; 006500.
 PR 07-APR-1997; US-667777.
 PA (WEBB/) WEBBER R.
 PT Webber R;
 DR WPI: 98-594495/50.

PR Detection of human inducible nitric oxide synthase - using an
 PR immunoassay in which a sample is contacted with a specific binding
 PR entity reactive with human iNOS or mimics.
 PS Example 4; Page 36; 93PP; English.
 CC This invention describes an immunoassay method where a sample with a
 CC specific binding entity (e.g., a monoclonal antibody) reactive to human
 CC inducible nitric oxide synthase (iNOS) or mimics of this protein is used
 CC to detect the presence of human iNOS protein in the sample. The method
 CC can be used for the detection and quantitation of human iNOS in cells and
 CC tissues for various pathophysiological conditions such as sepsis, septic
 CC shock, myocardial infarction, rejection of tissue in organs following
 CC transplantation, monitoring "flare ups" in certain autoimmune diseases
 CC such as lupus, psoriasis, and multiple sclerosis. This sequence
 CC represents a peptide from human iNOS which is used in the method of the
 CC invention.
 SQ Sequence 6 AA;

Query Match 57.1%; Score 20; DB 1; Length 6;
 Best Local Similarity 100.0%; Pred. No. 1.5e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VTQD 4
 |||||
 DB 3 VTQD 6

Search completed: June 30, 2000, 14:52:32
 Job time: 5999 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 30, 2000, 13:27:55 ; Search time 50.08 Seconds

(without alignments)
8.195 Million cell updates/secTitle: US-08-833-506c-89
Perfect score: 35
Sequence: 1 vTQDDLQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 168808 seqs, 58629743 residues

Total number of hits satisfying chosen Parameters: 2577

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : PIR_53:*

- 1: pir1:*
- 2: pir2:*
- 3: pir3:*
- 4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	21	60.0	7	2	S68004	hucolin, 75K chain acetylcholine race P51 complex suban
2	20	57.1	12	2	I33390	calnexin - mouse (anti protein - pha outer membrane por
3	20	57.1	15	2	E59819	outer membrane por
4	19	54.3	11	2	A55394	photosystem II oxy
5	18	51.4	12	2	B58503	myosin heavy chain
6	18	51.4	14	2	I40102	gallbladder stone
7	17	48.6	13	2	A21694	24K protein 4413 -
8	17	48.6	13	2	A57789	phospholipase C-be
9	17	48.6	13	2	P0218	biotin A - Citroba
10	17	48.6	15	2	B41047	hypothetical 8 pro
11	17	48.6	15	2	I40697	T-cell receptor be
12	16	45.7	4	2	PC4131	yolk glycoprotein
13	16	45.7	8	2	S29789	cytochrome P450 17
14	16	45.7	11	2	PH0904	F420-non-reducing-
15	16	45.7	12	2	S55681	potassium channel
16	16	45.7	12	2	B33800	hypothetical prote
17	16	45.7	13	2	S39762	translational elonga
18	16	45.7	13	2	S41209	hypothetical pro
19	16	45.7	14	2	PS0443	hexokinase (EC 2.7
20	16	45.7	15	2	P0002	lipoprotein lipase
21	16	45.7	15	2	I50116	chlorophyll /b/bi
22	16	45.7	15	2	PH1310	virg protein - Agr
23	16	45.7	15	2	B2501	actin 7 - soybean
24	15	42.9	9	2	S1324	25K elastin bindin
25	15	42.9	10	2	S15755	Dp116 - human
26	15	42.9	13	2	A41589	Ig heavy chain DJ
27	15	42.9	14	2	A41514	GMR02
28	15	42.9	14	2	I50116	leucosulfakinin-II
29	15	42.9	15	2	PH1310	
30	15	42.9	15	2		

ALIGNMENTS

31	15	42.9	15	2	S31219	30K protein - bovi
32	15	42.9	15	2	A42413	Ig heavy chain V r
33	14	40.0	14	2	JH0714	neuropeptide TE-6
34	14	40.0	14	2	S16165	opacity protein P.
35	14	40.0	14	2	B33045	calsequestrin fas
36	14	40.0	14	2	A61328	trypsin (EC 3.4.21)
37	14	40.0	14	2	PQ0726	Unidentified 4.5/4
38	14	40.0	14	2	I44644	neurotoxin-associ
39	14	40.0	14	2	S35490	type II Site Speci
40	14	40.0	14	2	PS0577	31K protein 3208 -
41	14	40.0	14	2	A61512	variant surface 91
42	14	40.0	14	2	G42762	multicatlytic end
43	14	40.0	14	2	S43877	heat-shock protein
44	14	40.0	14	2	I29501	beta-glucosidase (
45	14	40.0	14	2	PT0205	T cell receptor al
46	14	40.0	14	2	F48394	glycoprotein compo
47	14	40.0	14	2	A39103	tubulin beta-3 cha
48	14	40.0	14	2	PC4268	alpha-globulin - I
49	14	40.0	14	2	S29487	Gm-binding protei
50	14	40.0	14	2	PT0601	fibrinopeptide A -
51	14	40.0	14	2	PT0533	insulin-like grow
52	14	40.0	14	2	PH1631	IG H chain V-D-J r
53	14	40.0	14	2	G35141	T-cell receptor de
54	14	40.0	14	2	A31902	bone acidic glycop
55	14	40.0	14	2	D51226	light-harvesting p
56	13	37.1	5	2	PT0601	T-cell receptor be
57	13	37.1	6	2	PT0533	T-cell receptor be
58	13	37.1	7	2	S13630	ribosomal protein
59	13	37.1	7	2	PT0628	T-cell receptor be
60	13	37.1	7	2	PT0576	T-cell receptor be
61	13	37.1	9	2	PT0562	T-cell receptor be
62	13	37.1	9	2	PH0937	T-cell receptor be
63	13	37.1	9	2	A55784	fibroblast growth
64	13	37.1	10	2	S30572	T-cell receptor be
65	13	37.1	10	2	I41978	calliflRFAamide 9-
66	13	37.1	11	2	S31065	ornithine decarbox
67	13	37.1	11	2	A35243	H-hyoscyamin - Ja
68	13	37.1	12	2	S351737	T-cell Receptor be
69	13	37.1	12	2	S04013	lignin peroxidase
70	13	37.1	13	2	S04014	lignin peroxidase
71	13	37.1	13	2	B61458	Ig kappa chain V-I
72	13	37.1	13	2	S61576	Ig kappa chain V-I
73	13	37.1	13	2	PS5090	ribosomal protein
74	13	37.1	14	2	PH1615	chlorophyll a/b/bi
75	13	37.1	14	2	PT0615	IG H chain V-D-J r
76	13	37.1	14	2	PN0572	T-cell receptor be
77	13	37.1	15	2	PA0093	integrin host f
78	13	37.1	15	2	S57584	enamin synthetas
79	13	37.1	15	2	PA0062	fumarate hydratase
80	13	37.1	15	2	PA0088	protein QP200051 -
81	13	37.1	15	2	PN0144	serine proteinase
82	13	37.1	15	2	I50503	agrin - electric r
83	13	37.1	15	2	PT0679	glycoprotein - log
84	13	37.1	15	2	PC4127	T-cell receptor V-
85	13	37.1	15	2	B33640	collagen type I -
86	13	37.1	15	2	E45037	cerebellar degener
87	13	37.1	15	2	PT0722	formylglycarnide
88	13	37.1	15	2	S08301	T-cell receptor be
89	12	34.3	8	2	S29272	T-cell receptor be
90	12	34.3	8	2	S69165	tocopherol-binding
91	12	34.3	6	2	B41978	ferredoxin a2 - Ja
92	12	34.3	7	2	A12016	calliflRFAamide 2 -
93	12	34.3	7	2	PH0109	calliflRFAamide 3 -
94	12	34.3	8	2	PT0657	late G1-69 protein
95	12	34.3	8	2	GMR02	leucosulfakinin-II
96	12	34.3	8	2		
97	12	34.3	9	2		
98	12	34.3	9	2		
99	12	34.3	9	2		
100	12	34.3	10	1		

RESULT 1
S68004 huolin, 75K chain - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
C;Accession: S68004
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-7 <EDG>

Query Match Score 21; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+05
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDDQ 7
Db 4 DDDQ 7

RESULT 2
I33190 acetylcholine receptor (alternative exon 5b) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 30-May-1997
R;Mikhovilovic, M.; Mai, Y.; Herbstreith, M.; Rubboli, F.; Tarroni, P.; Clementi, F.; Ros
Biochem. Biophys. Res. Commun. 197, 137-144, 1993
A;Title: Splicing of an anti-sense Alu sequence generates a coding sequence variant for
A;Reference number: I33190; MUID:94071933
A;Status: preliminary; translation not shown
A;Molecule type: mRNA
A;Residues: 1-12 <RES>
A;Cross references: GB:L1143; PID:9441144
C;Keywords: alternative splicing; neurotransmitter receptor

Query Match Score 20; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 2e+02
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VTTQDDL 6
Db 6 VTTQGV 12

RESULT 3
E56819 PS I complex subunit 8 - cucumber (fragment)
C;Species: Cucumis sativus (cucumber)
C;Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 05-Jan-1996
R;Iwasaki, Y.; Ishikawa, H.; Hibino, T.; Takabe, T.
Biochim. Biophys. Acta 1059, 141-148, 1991
A;Title: Characterization of genes that encode subunits of cucumber PS I complex by N-t
A;Reference number: A56819; MUID:91355209
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <SIWA>
A;Note: sequence extracted from NCBI backbone (NCBIP:58606)

Query Match Score 20; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 2.5e+02;

Qy 1 VTTQDD 5
Db 10 VTTQDD 14

RESULT 4
A53594 calnexin - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 17-Mar-1999
C;Accession: A53594
R;Lanter, M.; Vestweber, D.
J. Biol. Chem. 268, 12263-12268, 1994
A;Title: The integrin chains beta-1 and alpha-6 associate with the chaperone calnexin
A;Reference number: A53594; MUID:94216347
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-15 <LEN>
C;Keywords: endoplasmic reticulum; molecular chaperone

Query Match Score 20; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VTTQDDL 6
Db 10 TTEDDL 15

RESULT 5
S42449 anti protein - phage P7
C;Species: Phage P7
C;Date: 07-Sep-1994 #sequence_revision 26-May-1995 #text_change 08-Oct-1999
R;Clitron, M.; Schuster, H.
Cell 62, 591-598, 1990
A;Title: The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.
A;Reference number: S42448; MUID:90335968
A;Accession: S42449
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-11 <CIT>
A;Cross-references: EMBL:M35139; NID:9215705; PID:9215707

Query Match Score 19; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.9e+02
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTTQDDL 6
Db 6 VTRNDI 11

RESULT 6
B55503 outer membrane porin protein OprD homolog - unidentified bacterium (fragment)
C;Species: unidentified bacterium
C;Accession: B55503
R;Binette, J.-P.; Binette, M.B.
submitted to the Protein Sequence Database, October 1996
A;Description: The proteins of kidney and gallbladder stones.
A;Reference number: A58503
A;Accession: B58503
A;Status: preliminary
A;Molecule type: protein

A; Residues: 1-12 <BIN>
 A; Experimental source: human bile with stones
 A; Note: sequenced along with secondary sequence MXIGNVNEKL

Query Match 51.4%; Score 18; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 5.2e+02;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TQDD 5

Db 2 QDD 5

RESULT 7

A61002 photosystem II oxygen evolving complex protein 1 - common tobacco (fragment)
 N; Alternate names: thylakoid membrane protein

C; Species: Nicotiana tabacum (common tobacco)
 C; Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 17-Mar-1999

C; Accession: A61002 R; Bauw, G.; Rasmussen, H.H.; Van Den Bulcke, M.; Van Damme, J.; Puype, M.; Gesser, B.; C; Electrophoresis 11, 52A-536, 1990

A; Title: Two-dimensional gel electrophoresis, protein electroblotting and microsequencing
 A; Reference number: A61002; MUID:91031404

A; Molecule type: Protein

A; Residues: 1-14 <B&D>
 C; Keywords: chloroplast; membrane protein; photosynthesis; photosystem II; thylakoid

Query Match 51.4%; Score 18; DB 2; Length 14;
 Best Local Similarity 42.9%; Pred. No. 6.2e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VTQDDLQ 7

Db 7 LTFDEIQ 13

RESULT 8

A23694 myosin heavy chain, smooth muscle - chicken (fragment)
 C; Species: Gallus gallus (chicken)

C; Date: 04-Oct-1991 #sequence_revision 04-Oct-1991 #text_change 07-Feb-1997
 C; Accession: A23694 R; Cole, D.G.; Yount, R.G.

J. Biol. Chem. 265, 22537-22546, 1990
 A; Title: Photolabelling of the 6 and 10 S conformations of gizzard myosin with 3' (2')-O-(

A; Reference number: A23694; MUID:91093105
 A; Accession: A23694
 A; Status: preliminary

A; Molecule type: protein
 A; Residues: 1-13 <COL>
 C; Keywords: smooth muscle

Query Match 48.6%; Score 17; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 9.3e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QDD 5

Db 11 QDD 13

RESULT 9

A57789 gallbladder stone matrix protein 1, 41K - human (fragment)
 C; Species: Homo sapiens (man)

C; Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 03-May-1996
 C; Accession: A57789 R; Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, February 1996
 A; Description: The Proteins of gallbladder stones.
 A; Reference number: A57789

A; Status: preliminary

A; Molecule type: protein

A; Experimental source: two gallbladder, one bladder, one kidney stone of different pa

A; Note: 9-leu and 12-Lys were also found

A; Note: 9-leu

A; Note: 12-Lys

Query Match 48.6%; Score 17; DB 2; Length 13;

Best Local Similarity 100.0%; Pred. No. 9.3e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QDD 5

Db 3 QDD 5

RESULT 10

PS0218 24K protein 4413 - rice (strain Nihonbare) (fragment)

N; Alternative names: unidentified protein QR310029
 C; Species: Oryza sativa (rice)

C; Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Aug-1997
 C; Accession: PS0218; PC4270
 R; Tsugita, A.

A; Submitted to JIPID, April 1993

A; Reference number: PS0206

A; Molecule type: protein

A; Accession: PS0218

A; Status: 1-15 <TSU>

A; Experimental source: strain Nihonbare

A; Note: molecular weight 24K, PI 6.0

R; Kawakami, T.; Kamo, M.; Chen, M.C.; Tsugita, A.
 A; Submitted to JIPID, April 1997
 A; Reference number: PC4267
 A; Accession: PC4270
 A; Molecule type: protein

A; Residues: 1-15 <KAW>

Query Match 48.6%; Score 17; DB 2; Length 15;

Best Local Similarity 75.0%; Pred. No. 1.1e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTDQ 4

Db 1 LRDQ 4

RESULT 11

B48047 phospholipase C-beta 4, PLC-retA - bovine (fragment)

C; Species: Bos primigenius taurus (cattle)

C; Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
 C; Accession: B48047 R; Lee, C.W.; Park, D.J.; Lee, K.H.; Kim, C.G.; Rhee, S.G.

J. Biol. Chem. 268, 21318-21327, 1993
 A; Title: Purification, molecular cloning, and sequencing of phospholipase C-beta 4.
 A; Reference number: A48047; MUID:94012687
 A; Accession: B48047
 A; Status: preliminary

A; Molecule type: protein

A; Residues: 1-15 <LEE>

A; Experimental source: retina

A; Note: sequence extracted from NCBI backbone (NCBIP:138522)

Query Match 48.6%; Score 17; DB 2; Length 15;

Best Local Similarity 57.1%; Pred. No. 1.1e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VTTQDDLQ 7 Query Match Score 45.7%; Score 16; DB 2; Length 11;
 Db 3 VTVEDEQ 9 Best Local Similarity 50.0%; Pred. No. 1.3e+03; Mismatches 1; Indels 0; Gaps 0;

RESULT 12

I40697 T-cell receptor beta chain V-D-J region (hybridoma S22C2) - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Accession: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
 R:Gold, D.P.; Offner, H.; Sun, D.; Willey, S.; Vandembark, A.A.; Wilson, D.B.
 J:Exp. Med.: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
 A:Reference number: PH0904
 A:Molecule type: mRNA
 A:Residues: 1-11 <GOL>
 A:Experimental source: myelin basic protein-immunized T-cell
 C:Keywords: T-cell receptor

Qy 2 TQDDLQ 7 Query Match Score 45.7%; Score 16; DB 2; Length 11;
 Db 3 SSDSLQ 8 Best Local Similarity 50.0%; Pred. No. 1.3e+03; Mismatches 1; Indels 0; Gaps 0;

RESULT 15

S55681 yolk glycoprotein 42K - chicken
 C:Species: Gallus gallus (chicken)
 C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
 C:Accession: S55681
 C:Yamamura, J.; Adachi, T.; Aoki, N.; Nakamura, R.; Matsuda, T.
 Biochim. Biophys. Acta 1244, 384-394, 1995
 A:Title: Precursor-product relationship between chicken vitellogenin and the yolk pro
 A:Reference number: S55680; MUID:95322425

A:Accession: S55681
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-12 <YAN>
 C:Keywords: glycoprotein

Qy 2 VTTQDD 5 Query Match Score 45.7%; Score 16; DB 2; Length 12;
 Db 1 TTDD 4 Best Local Similarity 40.0%; Pred. No. 1.4e+03; Mismatches 1; Indels 0; Gaps 0;

RESULT 16

S39762 cytochrome P450 UT-7b - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Accession: S39762
 C:Ohishi, N.; Inouka, S.; Suzuki, T.; Funae, Y.
 Biochim. Biophys. Acta 1158, 227-236, 1993
 A:Title: Characterization of two P-450 isozymes placed in the rat CYP2D subfamily
 A:Reference number: S39761; MUID:94072607
 A:Accession: S39762
 A:Molecule type: protein
 A:Residues: 1-12 <OH1>

Qy 2 TQDD 6 Query Match Score 45.7%; Score 16; DB 2; Length 12;
 Db 1 DDL 8 Best Local Similarity 40.0%; Pred. No. 1.4e+03; Mismatches 0; Indels 0; Gaps 0;

RESULT 17

S41209 FA20-non-reducing-hydrogenase (EC 1.12.99.-) 17K chain - Methanobacterium thermoautot
 C:Species: Methanobacterium thermoautotrophicum
 C:Variety: strain Marburg
 C:Accession: S41209
 R:Seitz, E.; Heiderich, R.; Heiden, S.; Thauer, R.K.
 Eur. J. Biochem. 220, 139-148, 1994
 A:Title: H(2)-heterodisulfide oxidoreductase complex from Methanobacterium thermoaut
 A:Reference number: S41204; MUID:94164153

A;Accession: S41209
A;Molecule type: protein
A;Residues: 1-13 <SER>
A;Experimental source: strain Marburg
C;Complex: membrane-associated complex; holoenzyme is the hydrogen: heterodisulfide oxidoreductase (EC 1.12.99.-) and a F420-non-reducing-hydrogenase (EC 1.12.99.-) subcomplex; each of the subcomplexes (EC 1.12.99.2) and a F420-non-reducing-hydrogenase (EC 1.12.99.-) subcomplex; each of the subcomplexes (EC 1.12.99.2) and a F420-non-reducing-hydrogenase (EC 1.12.99.-) subcomplex; each of the subcomplexes (EC 1.12.99.2)
C;Function: reduction of coenzyme M-N-7-mercaptopropanoylthreonine phosphate heterodisulfide (EC 1.12.99.2)
A;Description: reduction of coenzyme M-N-7-mercaptopropanoylthreonine phosphate heterodisulfide (EC 1.12.99.2)
C;Keywords: membrane-associated complex; oxidoreductase

Query Match Score 45.7%; Pred. No. 1.5e+03; Length 13;
Best Local Similarity 50.0%; Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 QDDL 6
Db 2 ERDI 5

RESULT 18
PS0443 potassium channel protein Slo G3 - fruit fly (*Drosophila melanogaster*) (fragment)
C;Species: *Drosophila melanogaster*
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Feb-1997
C;Accession: PS0443
R;Adelman, J.P.; Shen, K.Z.; Kavanaugh, M.P.; Warren, R.A.; Wu, Y.N.; Lagrutta, A.; Bond Neuron 9, 209-216, 1992
A;Title: Calcium-activated potassium channels expressed from cloned complementary DNAs.
A;Reference number: JH0697; MUID:92360298
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-13 <ADE>
C;Comment: This potassium channel is activated by calcium.
C;Genetics:
A;Gene: FlyBase:slo
A;Cross-references: FlyBase:FBgn0003429
C;Keywords: alternative splicing; ion channel; potassium channel; transmembrane protein

Query Match Score 45.7%; Pred. No. 1.5e+03; Length 13;
Best Local Similarity 100.0%; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
Db 10 DDL 12

RESULT 19
S29789 hypothetical protein - *Thermoplasma acidophilum* (fragment)
C;Species: *Thermoplasma acidophilum*
C;Date: 25-Feb-1994 #sequence_revision 26-May-1995 #text_change 26-May-1995
C;Accession: S29789
R;Bright, J.R.; Bryson, D.; Danson, M.J.; Hough, D.W.; Towner, P.
A;Title: Cloning, sequencing and expression of the gene encoding glucose dehydrogenase f
A;Reference number: S29788; MUID:93170285
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-14

A;Cross-references: ENBL:259788

Query Match Score 45.7%; Pred. No. 1.6e+03; Length 14;
Best Local Similarity 100.0%; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6

RESULT 20
PA0110 translation elongation factor eEF-1 beta' chain - *Arabidopsis thaliana* (fragment)
C;Species: *Arabidopsis thaliana* (mouse-ear cress)
C;Accession: PA0110
R;Kamo, M.; Kawakami, T.; Tsugita, A.
A;Submitted to JIPID, March 1995
A;Reference number: PA0109
A;Molecule type: protein
A;Residues: 1-15 <KAM>

Query Match Score 45.7%; Pred. No. 1.8e+03; Length 15;
Best Local Similarity 66.7%; Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VTQDDL 6
Db 2 VTFSDL 7

RESULT 21
B32800 hypothetical protein (P1 5' region) - human (fragment)
C;Species: *Homo sapiens* (man)
C;Accession: B32800
R;Jindal, S.; Budani, A.K.; Singh, B.; Harley, C.B.; Gupta, R.S.
Mol. Cell. Biol. 9, 2279-2283, 1989
A;Title: Primary structure of a human mitochondrial protein homologous to the bacteriophage lambda N protein
A;Reference number: A32800; MUID:89313783
A;Accession: B32800
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-15 <JIN>
A;Cross-references: GB:M22382

Query Match Score 45.7%; Pred. No. 1.8e+03; Length 15;
Best Local Similarity 100.0%; Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
Db 1 DDL 3

RESULT 22
C32521 hexokinase (EC 2.7.1.1) I Peptide II - rat (fragment)
C;Species: *Rattus norvegicus* (Norway rat)
C;Accession: C32521
R;Schirch, D.M.; Wilson, J.E.
Arch. Biochem. Biophys. 257, 1-12, 1987
A;Title: Rat brain hexokinase: amino acid sequence at the substrate hexose binding site
A;Reference number: A90080; MUID:87324917
A;Accession: C32521
A;Molecule type: protein
A;Residues: 1-15 <SCHE>
C;Keywords: glycolysis; phosphotransferase

Query Match Score 45.7%; Pred. No. 1.8e+03; Length 15;
Best Local Similarity 75.0%; Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 DDL 6

A; Status: preliminary; translated from GB/EMBL/DDJB
A; Molecule type: mRNA
A; Residues: 1-14 <RES>
A; Cross-references: GB:MI18187; NID:9192097; PID:AAA37272.1; PID:9192098

Query Match 42.9%; Score 15; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DLQ 7
 | | |
Db 3 DLQ 5

RESULT 29

158116 - human
DP116 - Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 13-Aug-1999
C;Accession: 158116
R;Byers, T.J.; Lidov, H.G.; Kunkel, L.M.
N;Nature Gener. 4, 77-81, 1993
A;Title: An alternative dystrophin transcript specific to peripheral nerve.
A;Reference number: 158116; MUID:93991881
A;Accession: 158116
A;Status: preliminary; translated from GB/EMBL/DDJB
A;Molecule type: mRNA
A;Residues: 1-15 <RES>
A;Cross-references: GB:SG62617; NID:9386224; PID:ABA27159.1; PID:9386225
C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin

Query Match 42.9%; Score 15; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 DLQ 7
 | | |
Db 11 DLQ 13

RESULT 30

PH1310
19 heavy chain DJ region (clone C770-107) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C;Accession: PH1310
R;Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A;Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A;Reference number: PH1302; MUID:93094761
A;Accession: PH1310
A;Molecule type: DNA
A;Residues: 1-15 <WAS>
C;Keywords: heterotetramer; immunoglobulin

Query Match 42.9%; Score 15; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TQDDL 6
 | | |
Db 1 TGDEL 5

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: June 30, 2000, 14:52:37 ; Search time 39.08 Seconds
(without alignments)
5.455 Million cell updates/sec

Title: US-08-833-506C-89

Perfect score: 35 Gapext 0.5
Scoring table: BLOSUM62

Sequence: 1 vtdDLQ 7

Searched: 83857 seqs., 30454973 residues

Total number of hits satisfying chosen Parameters: 668

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match 0%

Listing first 100 summaries

Database : SwissProt_38:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	20	57.1	15	1	PSO_CUCSA	P42052 cucumis sat
2	17	48.6	5	1	BIOA_CITFR	P12071 citrobacter
3	17	48.6	5	1	BIOA_SALTY	P12677 salmonella
4	17	48.6	9	1	UFO2_MOUSE	P38640 mus musculu
5	16	45.7	12	1	XYL_A_STRAVC	P14405 streptomyce
6	16	45.7	14	1	YGDH_THERAC	Q05213 thermoplasm
7	15	42.9	11	1	UFO5__MOUSE	P38643 mus musculu
8	15	42.9	13	1	ACT_SOYBN	P15987 glycine max
9	15	42.9	14	1	GLGS_SPOL	P55235 spinacia ol
10	14	40.0	10	1	UXA7_CHIUR	P38008 chlamydia t
11	14	40.0	11	1	T2P__PROVOL	P31031 proteus vul
12	14	40.0	12	1	UPO1_CABEP	P55954 caenorhabdi
13	14	40.0	13	1	UNO2_PINBS	P81667 pinus pinas
14	14	40.0	14	1	RECU_SALTY	P28355 salmonella
15	14	40.0	15	1	FKB7_PINBS	P81104 pinus pinas
16	13	37.1	11	1	FAR9_CALVO	P41864 calliphora
17	13	37.1	12	1	LOSS_LOCMI	P47733 locusta mig
18	13	37.1	12	1	ULAL_MOUSE	P99032 mus musculu
19	13	37.1	13	1	EP65_HUMAN	P54963 homo sapien
20	13	37.1	13	1	LIGA_TRAVE	P20011 trameutes ve
21	13	37.1	13	1	LIGB_TRAVE	P20012 trameutes ve
22	13	37.1	13	1	RL30_SALTY	O54300 salmonella
23	13	37.1	14	1	HCYA_MEGRU	Q10583 megatheria c
24	13	37.1	15	1	ITRB_ALBUJU	P24927 albizzia ju
25	13	37.1	15	1	RKGG_CARCER	P21586 careta car
26	13	37.1	15	1	UNO1_PINBS	P201106 pinus pinas
27	12	34.3	9	1	FAR2_CALVO	P41857 calliphora
28	12	34.3	9	1	FAR3_CALVO	P4158 calliphora
29	12	34.3	9	1	NSKI_SARCO	P41492 sarcophaga
30	12	34.3	9	1	UHA2_HUMAN	P40929 homo sapien
31	12	34.3	9	1	ULAH_HUMAN	P31934 homo sapien
32	12	34.3	10	1	FARC_CALVO	P24867 calliphora
33	12	34.3	10	1	FIBB_CERSI	P14537 ceratotheri
34	12	34.3	10	1	GS09_BACSU	P80243 bacillus su

ALIGNMENTS

RESULT 1
PSAO_CUCSA

ID	PSAO_CUCSA	STANDARD;	PRT;	15 AA.		CC	-----
AC	P42052;					DR	ENBL: M21922; CAB25179.1;
DT	01-NOV-1995 (Rel. 32, Created)					DR	PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
DT	01-NOV-1995 (Rel. 32, Last sequence update)					KW	Biotin biosynthesis; Transferase; Aminotransferase;
DT	01-NOV-1995 (Rel. 32, Last annotation update)					KW	Pyridoxal phosphate.
DE	PHOTOSYSTEM I REACTION CENTRE SUBUNIT 8 (PHOTOSYSTEM I 17.5 KD PROTEIN) (FRAGMENT).					NON_TER	5
GN	PSM.					SEQUENCE	5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
OS	Cucumis sativus (Cucumber).					QY	1 VTIQDD 5
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;					DB	1 MTIIDD 5
OC	euphyllophytes; Spermatophyta; Magnoliophyta; eudicots; core eudicots; Rosidae; eurosids I; Cucurbitales; Cucurbitaceae;						
OC	Cucumis.						
RN	[1]						
RP	SEQUENCE.						
RC	TISSUE=COBYLEDON;						
RX	MEDLINE: 91355209.						
RA	Iwasaki Y., Ishikawa H., Hibino T., Takabe T.;						
RT	"Characterization of genes that encode subunits of cucumber PS I complex by N-terminal sequencing";						
RT	Biochim Biophys Acta 1059:141-148 (1991).						
CC	-I- FUNCTION: ESSENTIAL FOR THE ACTIVITY OF NADP PHOTOREDUCTION.						
RL	KW Photosystem I; Photosynthesis; Chloroplast; Thylakoid membrane.						
FT	NON_TER 15						
SQ	SEQUENCE 15 AA; 1714 MW; CA0BF5DAD403D9F4 CRC64;						
Query Match	57.1%; Score 20; DB 1; Length 15;						
Best Local Similarity	80.0%; Pred. No. 1.2e+02;						
Matches	4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;						
QY	1 VTIQDD 5						
DB	10 VTIQDD 14						
RESULT	2						
BIOA_CITFR	STANDARD;	PRT;	5 AA.			CC	-----
ID	BIOA_CITFR	STANDARD;	PRT;	5 AA.		DR	ENBL: M21922; CAB2518.1;
AC	P13071;					DR	PROSITE; SG10026; BIOM.
DT	01-JAN-1990 (Rel. 13, Created)					DR	STYGENE; SG10026; BIOM.
DT	01-JAN-1990 (Rel. 13, Last sequence update)					DR	PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
DT	01-DEC-1992 (Rel. 24, Last annotation update)					KW	Biotin biosynthesis; Transferase; Aminotransferase;
DE	ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (DAPA DE (EC 2.6.1.62) (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA DE AMINOTRANSFERASE) (FRAGMENT).					KW	Pyridoxal phosphate.
DE	(EC 2.6.1.62) (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA DE AMINOTRANSFERASE) (FRAGMENT).					NON_TER	5
GN	BIOA.					SEQUENCE	5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
OC	Citrobacter freundii.					CC	-----
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RN	[1]					CC	-----
RP	SEQUENCE FROM N.A.					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
RX	MEDLINE: 89006280.					CC	-----
RA	Shiu D., Campbell A.;					DR	ENBL: M21922; CAB2518.1;
RT	"Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundii and Salmonella typhimurium biotin operons."					DR	PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
RT	Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundii and Salmonella typhimurium biotin operons."					KW	Biotin biosynthesis; Transferase; Aminotransferase;
RT	Gene 67:203-211(1998).					KW	Pyridoxal phosphate.
RI	7,8-DIAMINONONANOATE.					NON_TER	5
CC	-I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-OXONONANOATE - S-ADENOSYL-4-METHYLTHIO-2-OXBUTANOATE + 7,8-DIAMINONONANOATE.					SEQUENCE	5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
CC	-I- COFACTOR: PYRIDOXAL PHOSPHATE.					CC	-----
CC	-I- PATHWAY: BIOTIN BIOSYNTHESIS.					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	-I- SUBUNIT: HOMODIMER.					CC	-----
CC	-I- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.					CC	-----
CC	Citrobacter.					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	SEQUENCE FROM N.A.					CC	-----
CC	Shiu D., Campbell A.;					DR	ENBL: M21922; CAB2518.1;
CC	"Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundii and Salmonella typhimurium biotin operons."					DR	PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
CC	Gene 67:203-211(1998).					KW	Biotin biosynthesis; Transferase; Aminotransferase;
CC	-I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-OXONONANOATE - S-ADENOSYL-4-METHYLTHIO-2-OXBUTANOATE + 7,8-DIAMINONONANOATE.					KW	Pyridoxal phosphate.
CC	-I- COFACTOR: PYRIDOXAL PHOSPHATE.					NON_TER	5
CC	-I- PATHWAY: BIOTIN BIOSYNTHESIS.					SEQUENCE	5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
CC	-I- SUBUNIT: HOMODIMER.					CC	-----
CC	-I- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.					CC	-----
CC	Citrobacter.					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	SEQUENCE FROM N.A.					CC	-----
CC	Shiu D., Campbell A.;					DR	ENBL: M21922; CAB2518.1;
CC	"Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundii and Salmonella typhimurium biotin operons."					DR	PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
CC	Gene 67:203-211(1998).					KW	Biotin biosynthesis; Transferase; Aminotransferase;
CC	-I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-OXONONANOATE - S-ADENOSYL-4-METHYLTHIO-2-OXBUTANOATE + 7,8-DIAMINONONANOATE.					KW	Pyridoxal phosphate.
CC	-I- COFACTOR: PYRIDOXAL PHOSPHATE.					NON_TER	5
CC	-I- PATHWAY: BIOTIN BIOSYNTHESIS.					SEQUENCE	5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
CC	-I- SUBUNIT: HOMODIMER.					CC	-----
CC	-I- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.					CC	-----
CC	Citrobacter.					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	SEQUENCE FROM N.A.					CC	-----
CC	Shiu D., Campbell A.;					DR	ENBL: M21922; CAB2518.1;
CC	"Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundii and Salmonella typhimurium biotin operons."					DR	PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
CC	Gene 67:203-211(1998).					KW	Biotin biosynthesis; Transferase; Aminotransferase;
CC	-I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-OXONONANOATE - S-ADENOSYL-4-METHYLTHIO-2-OXBUTANOATE + 7,8-DIAMINONONANOATE.					KW	Pyridoxal phosphate.
CC	-I- COFACTOR: PYRIDOXAL PHOSPHATE.					NON_TER	5
CC	-I- PATHWAY: BIOTIN BIOSYNTHESIS.					SEQUENCE	5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
CC	-I- SUBUNIT: HOMODIMER.					CC	-----
CC	-I- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.					CC	-----
CC	Citrobacter.					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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CC	Gene 67:203-211(1998).					KW	Biotin biosynthesis; Transferase; Aminotransferase;
CC	-I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-OXONONANOATE - S-ADENOSYL-4-METHYLTHIO-2-OXBUTANOATE + 7,8-DIAMINONONANOATE.					KW	Pyridoxal phosphate.
CC	-I- COFACTOR: PYRIDOXAL PHOSPHATE.					NON_TER	5
CC	-I- PATHWAY: BIOTIN BIOSYNTHESIS.					SEQUENCE	5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
CC	-I- SUBUNIT: HOMODIMER.					CC	-----
CC	-I- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.					CC	-----
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CC	"Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundii and Salmonella typhimurium biotin operons."					DR	PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
CC	Gene 67:203-211(1998).					KW	Biotin biosynthesis; Transferase; Aminotransferase;
CC	-I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-OXONONANOATE - S-ADENOSYL-4-METHYLTHIO-2-OXBUTANOATE + 7,8-DIAMINONONANOATE.					KW	Pyridoxal phosphate.
CC	-I- COFACTOR: PYRIDOXAL PHOSPHATE.					NON_TER	5
CC	-I- PATHWAY: BIOTIN BIOSYNTHESIS.					SEQUENCE	5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
CC	-I- SUBUNIT: HOMODIMER.					CC	-----
CC	-I- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.					CC	-----
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CC	"Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundii and Salmonella typhimurium biotin operons."					DR	PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
CC	Gene 67:203-211(1998).					KW	Biotin biosynthesis; Transferase; Aminotransferase;
CC	-I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-OXONONANOATE - S-ADENOSYL-4-METHYLTHIO-2-OXBUTANOATE + 7,8-DIAMINONONANOATE.					KW	Pyridoxal phosphate.
CC	-I- COFACTOR: PYRIDOXAL PHOSPHATE.					NON_TER	5
CC	-I- PATHWAY: BIOTIN BIOSYNTHESIS.					SEQUENCE	5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
CC	-I- SUBUNIT: HOMODIMER.					CC	-----
CC	-I- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.					CC	-----
CC	Citrobacter.					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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CC	"Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundii and Salmonella typhimurium biotin operons."					DR	PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
CC	Gene 67:203-211(1998).					KW	Biotin biosynthesis; Transferase; Aminotransferase;
CC	-I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-OXONONANOATE - S-ADENOSYL-4-METHYLTHIO-2-OXBUTANOATE + 7,8-DIAMINONONANOATE.					KW	Pyridoxal phosphate.
CC	-I- COFACTOR: PYRIDOXAL PHOSPHATE.					NON_TER	5
CC	-I- PATHWAY: BIOTIN BIOSYNTHESIS.					SEQUENCE	5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
CC	-I- SUBUNIT: HOMODIMER.					CC	-----
CC	-I- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.					CC	-----
CC	Citrobacter.					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
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CC	Shiu D., Campbell A.;					DR	ENBL: M21922; CAB2518.1;
CC	"Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundii and Salmonella typhimurium biotin operons."					DR	PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
CC	Gene 67:203-211(1998).					KW	Biotin biosynthesis; Transferase; Aminotransferase;
CC	-I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-OXONONANOATE - S-ADENOSYL-4-METHYLTHIO-2-OXBUTANOATE + 7,8-DIAMINONONANOATE.					KW	Pyridoxal phosphate.
CC	-I- COFACTOR: PYRIDOXAL PHOSPHATE.					NON_TER	5
CC	-I- PATHWAY: BIOTIN BIOSYNTHESIS.					SEQUENCE	5 AA; 582 MW; 6AAAB1B1A6F00000 CRC64;
CC	-I- SUBUNIT: HOMODIMER.					CC	-----
CC	-I- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT AMINOTRANSFERASES.					CC	-----
CC	Citrobacter.					CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC	SEQUENCE FROM N.A.					CC	-----
CC	Shiu D., Campbell A.;					DR	ENBL: M21922; CAB2518.1;
CC	"Transcriptional regulation and gene arrangement of Escherichia coli, Citrobacter freundii and Salmonella typhimurium biotin operons."					DR	PROSITE; PS00600; AA_TRANSFER_CLASS_3; PARTIAL.
CC	Gene 67:203-211(1998).					KW	Biotin biosynthesis; Transferase; Aminotransferase;
CC	-I- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + 8-AMINO-7-OXONONANOATE - S-ADENOSYL-4-METHYLTHIO-2-OXBUTANOATE + 7,8-DIAMINONONANOATE.					KW	Pyridoxal phosphate.
CC	-I- COFACTOR: PYRIDOXAL PHOSPHATE.					NON_TER	5
CC	-I- PATHWAY: BIOTIN BIOSYNTHESIS.					SEQUENCE	5 AA; 582 MW; 6AAAB1B1A6F00000 CRC

RESULT 4
 ID UF02_MOUSE STANDARD; PRT; 9 AA.
 AC P8840;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P22) (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 RN [1]
 RP TISSUE=FIBROBLAST;
 RX MEDLINE; 95009907.
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RR "Separation and sequencing of familiar and novel murine Proteins
 using preparative two-dimensional gel electrophoresis.";
 RT Electrophoresis 15:735-745(1994).
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 6.0, ITS MW IS: 32 KD.
 FT NON-TER 9 9
 SQ SEQUENCE 9 AA; 1102 MW; 7E73EAB6D05B1AAB CRC64;

Query Match 48.6%; Score 17; DB 1; Length 9;
 Best Local Similarity 40.0%; Pred. No. 8.4e+04;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

RESULT 5
 ID XYLA_STRVN STANDARD; PRT; 12 AA.
 AC P14405;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE XYLOSE ISOMERASE (EC 5.3.1.5) (FRAGMENT).
 OS Streptomyces violaceoruber.
 OC Bacteria; Firmicutes; Actinobacteridae; Streptomycetaceae; Streptomyces.
 RN [1]
 RP SEQUENCE,
 RX STRAIN=LMG 7183;
 RA Vaughn-Sperre W., Ampe C., Kersters-Hilderson H., Tempst P.;
 RR "Single active-site histidine in D-xylose isomerase from Streptomyces
 violaceoruber. Identification by chemical derivatization and peptide
 mapping.";
 RL Biochem. J. 263:195-199(1989).
 CC -!- CATALYTIC ACTIVITY: D-XYLOSE = D-XYLULOSE.
 CC -!- COFACTOR: MAGNESIUM IS NECESSARY FOR THE ACTIVITY.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- SIMILARITY: BELONGS TO THE XYLOSE ISOMERASE FAMILY.
 DR HSSP; P37031; 1DXI.
 PROSITE; PS00172; XYLOSE_ISOMERASE_1; PARTIAL.
 DR PROSITE; PS00173; XYLOSE_ISOMERASE_2; PARTIAL.
 KW Isomerase; Pentose shunt; Xylose metabolism; Magnesium.
 FT NON-TER 1 1
 ACT SITE 5 5
 FT NON-TER 12 12
 SQ SEQUENCE 12 AA; 1375 MW; E749268E1AAAAA1 CRC64;

Query Match 45.7%; Score 16; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 6.6e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
 Db 7 DDL 9

RESULT 6
 ID YGDH_THRAC STANDARD; PRT; 14 AA.
 AC Q0213;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 01-JUN-1994 (Rel. 29, Last annotation update)
 DE HYPOTHETICAL PROTEIN IN GLUCOSE DEHYDROGENASE GENE 3' REGION
 (FRAGMENT).
 OS Thermoplasma acidophilum.
 OC Archaea; Euryarchaeota; Thermoplasmae; Thermoplasmae;
 OC Thermoplasma

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1728;
 RX MEDLINE; 93170285.
 RA Bright J.R., Byrom D., Danson M.J., Hough D.W., Towner P.;
 RT "Cloning, sequencing and expression of the gene encoding glucose
 dehydrogenase from the thermophilic archaeon Thermoplasma
 acidophilum.";
 RT EUR. J. Biochem. 211:549-554 (1993).
 CC ---
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 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>).
 CC or send an email to license@isb-sib.ch).

CC ---
 DR EMBL; X59788; CAA2451..1;
 DR PIR; S29789; S29789.
 KW Hypothetical protein.
 FT NON-TER 14 14
 SQ SEQUENCE 14 AA; 1674 MW; 685A1FFF26529944 CRC64;

Query Match 45.7%; Score 16; DB 1; Length 14;
 Best Local Similarity 100.0%; Pred. No. 7.8e+02;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 DDL 6
 Db 9 DDL 11

RESULT 7
 ID UF05_MOUSE STANDARD; PRT; 11 AA.
 AC P3643;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF FIBROBLASTS (P48) (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Rutherfordia; Rodentia; Sciurognathia; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE,
 RC TISSUE=FIBROBLAST;
 RX MEDLINE; 95009907.
 RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;
 RR "Separation and sequencing of familiar and novel murine proteins;
 using preparative two-dimensional gel electrophoresis.";
 RL Electrophoresis 15:735-745(1994)
 CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 PROTEIN IS: 5.5, ITS MW IS: 48 KD.

FT	NON_TER	11	11 AA;	1328 MW;	E54835E5AAABAFPA CRC64;	RESULT 9
SQ	SEQUENCE	11				GLOSG_SPOL
Query Match	Score 15;	DB 1;	Length 11;			ID GLOSG_SPOL
Best Local Similarity	42.9%	Pred. No. 9.7e+03;				ID P55235;
Matches 2;	Conservative	2; Mismatches 2;	Indels 0;	Gaps 0;		AC P55235;
Qy 1	VTDPLD 6					DT 01-OCT-1996 (Rel. 34, Created)
Db 3	IIXDDV 8					DT 01-OCT-1996 (Rel. 34, Last sequence update)
RESULT 8						DT 01-NOV-1997 (Rel. 35, Last annotation update)
ACT7_SOYBN	STANDARD;	PRT;	13 AA.			DE GLUCOSE-1-PHOSPHATE ADENYLTRANSFERASE SMALL SUBUNIT (EC 2.7.7.27)
ID ACT7_SOYBN	STANDARD;	PRT;	13 AA.			DE (ADP-GLUCOSE PYROPHOSPHORYLASE) (AGPASE B)
AC P15987;						DE (ALPHA-D-GLUCOSE-1-PHOSPHATE ADENYL TRANSFERASE) (FRAGMENT).
DT 01-APR-1990 (Rel. 14, Created)						OS Spinacia oleracea (spinach).
DT 01-APR-1990 (Rel. 14, Last sequence update)						OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophita; Magnoliophyta; eudicots; Malpighiales; Caryophyllidae; Caryophyllaceae; core eudicots; Caryophyllales; Chenopodiaceae; Spinacia; OC
DT 15-JUL-1999 (Rel. 38, Last annotation update)						OC
DE ACTIN 7 (FRAGMENT).						RN [1]
GN SACT.						RP
OS Glycine max (Soybean).						RC TISSUE=LEAF; Morell M.K., Bloom M., Knowles V., Preiss J.;
GC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Magnoliophyta; eudicots; Malpighiales; core eudicots; Rosidae; Eurosids I; Fabales; Fabaceae; Papilionoideae; Glycine.						RA "Subunit structure of spinach leaf ADPGlucose pyrophosphorylase.";
CC (1)						RA RT
RN SEQUENCE FROM N.A.						RL Plant Physiol. 83:182-187(1987).
RC STRAIN=CV_WAYNE;						CC -I FUNCTION: THIS PROTEIN PLAYS A ROLE IN SYNTHESIS OF STARCH.
RX MEDLINE: 91136640.						CC IT CATALYSES THE SYNTHESIS OF THE ACTIVATED GLYCOSYL DONOR.
RA Pearson L., Meagher R.B.;						CC -I ADP-GLUCOSE FROM GLC-1-P AND ATP.
RT "Diverse soybean actin transcripts contain a large intron in the 5' untranslated leader: structural similarity to vertebrate muscle actin genes."						CC -I CATALYTIC ACTIVITY: ATP + ALPHA-D-GLUCOSE 1-PHOSPHATE = PYROPHOSPHATE + ADP-GLUCOSE.
RT Plant Mol. Biol. 14:513-526(1990).						CC -I ENZYME REGULATION: ACTIVATED BY 3'-PHOSPHOGLYCERATE, INHIBITED BY ORTHOPHOSPHATE. ALLOSTERIC REGULATION.
CC -I FUNCTION: ACTINS ARE HIGHLY CONSERVED PROTEINS THAT ARE INVOLVED IN VARIOUS TYPES OF CELL MOTILITY AND ARE UNIQUITUOUSLY EXPRESSED IN ALL EUKARYOTIC CELLS.						CC -I PATHWAY: STARCH BIOSYNTHESIS.
CC -I FUNCTION: ESSENTIAL COMPONENT OF CELL CYTOSKELETON; PLAYS AN IMPORTANT ROLE IN CYTOPLASMIC STREAMING, CELL SHAPE DETERMINATION, CELL DIVISION, ORGANELLE MOVEMENT AND EXTENSION GROWTH.						CC -I SUBCELLULAR LOCATION: CHLOROPLAST; Chloroplast.
CC -I MISCELLANEOUS: THERE ARE AT LEAST 16 ACTIN GENES IN SOYBEAN.						CC -I SIMILARITY: BELONGS TO THE ACTIN FAMILY.
CC -I SIMILARITY: BELONGS TO THE ACTIN FAMILY.						CC PHOSPHATE ADENYLTRANSFERASE FAMILY.
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CC EMBL: X17120; CAA4980_1; -.						DR PROSITE; PS00809; ADP_GLC_PYROPHSP_2; PARTIAL.
CC PIR: S15755; S15755.						DR PROSITE; PS00810; ADP_GLC_PYROPHSP_3; PARTIAL.
CC PROSITE; PS00406; ACTINS_1; PARTIAL.						KW Glycogen biosynthesis; Transferase; Nucleotidyltransferase;
CC DR PROSITE; PS00432; ACTINS_2; PARTIAL.						KW Multigene family; Starch biosynthesis; Allosteric enzyme;
CC PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.						CC NON_TER 14 14
CC Structural protein; Multigene family.						SQ SEQUENCE 14 AA; 1490 MW; 98B5792C3AE73BC5 CRC64;
CC FT 13 AA;						Query Match Score 15; DB 1; Length 14; Best Local Similarity 60.0%; Pred. No. 1.3e+03; Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
CC CC Chlamydiae; Chlamydia.						CC TOPDL 6
CC DR RN [1]						DB 7 SDGQ 11
CC DR PIR: S15755; S15755.						RESULT 10
CC DR PROSITE; PS00406; ACTINS_1; PARTIAL.						UXA7_CHTR STANDARD; PRT; 10 AA.
CC DR PROSITE; PS00432; ACTINS_2; PARTIAL.						ID UXA7_CHTR
CC PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.						ID P38018;
CC KW Structural protein; Multigene family.						AC P38018;
CC FT 13 AA;						DT 01-OCT-1994 (Rel. 30, Created)
CC CC Chlamydiae; Chlamydia.						DT 01-OCT-1994 (Rel. 30, Last sequence update)
CC DR RN [1]						DT 15-FEB-2000 (Rel. 39, Last annotation update)
CC RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M., Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G., Pallini V.; Submitted (SEP-1994) to the SWISS-PROT data bank.						DE UNKNOWN PROTEIN FROM 2D-PAGE FROM ELEMENTARY BODY (FRAGMENT).
CC -I MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.65 OR 6.89 (TWO SPOTS ARE PRESENT), ITS MW IS: 70 KD.						OS Chlamydia trachomatis.
CC CC CC						OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
CC CC CC						RN [1]
CC DR PIR: S15755; S15755.						RP SEQUENCE.
CC DR PROSITE; PS00406; ACTINS_1; PARTIAL.						RC STRAIN=12/424/BU;
CC DR PROSITE; PS00432; ACTINS_2; PARTIAL.						RA Bini L., Santucci A., Magi B., Marzocchi B., Sanchez-Campillo M., Comanducci M., Christianen G., Birkelund S., Vretou E., Ratti G., Pallini V.; Submitted (SEP-1994) to the SWISS-PROT data bank.
CC DR PROSITE; PS01132; ACTINS_ACT_LIKE; PARTIAL.						RA -I MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN PROTEIN IS: 6.65 OR 6.89 (TWO SPOTS ARE PRESENT), ITS MW IS: 70 KD.
CC CC CC						RA CC CC CC
CC CC CC						DB 5 EDQ 8
CC CC CC						QY 4 DDQ 7

FT NON-TER 10 10 SQ 1251 MW; 80A43FD0D731AAB1 CRC64;

Query Match 40.0%; Score 14; DB 1; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 DRFLQ 7
Db 4 DRFLQ 7

RESULT 11 T2P1_PVU0V STANDARD; PRT; 11 AA.

ID T2P1_PVU0V STANDARD; PRT; 11 AA.

AC P31031; 1:
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE TYPE II RESTRICTION ENZYME PVU1 (EC 3.1.21.4) (ENDONUCLEASE PVU1)
DE (R PVU1) (FRAGMENT).
OS Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteobacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 13315;
RX MEDLINE; 9308718X.
RA Smith M.D., Longo M., Gerard G.F., Chatterjee D.K.;
RT "Cloning and characterization of genes for the PvuI restriction and
modification systems." (See http://www.isb-sib.ch/announce/
Nucleic Acids Res. 20:5743-5747(1992).
RL EMBL; 104163; AAC25660.1; -.
CC -!- CATALYTIC ACTIVITY: RECOGNIZES THE DOUBLE-STRANDED SEQUENCE CGATCG
AND CLEAVES AFTER T-4 .
CC -----
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or send an email to licensee@isb-sib.ch).
CC -----
DR PIR: S35490; S35490.
DR REBASE: RB0107; PvuI.
KW Hydrolase; Endonuclease; Nuclease; Restriction system.
FT NON-TER 1 1
SEQUENCE 11 AA; 1300 MW; 9E0CDE7955B72B1A CRC64;

Query Match 40.0%; Score 14; DB 1; Length 11;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VTODDL 6
Db 1 ISVDEL 6

RESULT 12 UP01_CAEEL STANDARD; PRT; 12 AA.

ID UP01_CAEEL STANDARD; PRT; 12 AA.

AC P5555; 1:
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE (SPOT 1) (FRAGMENT).
Caenorhabditis elegans; Metazoa; Nematoda; Secernentea; Rhabditida;
Rhabditina; Rhabditoldea; Pelederinae; Caenorhabditis.
OS Bacteria; proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella typhimurium;
RN [1]

RP SEQUENCE FROM N.A.

RP SEQUENCE.
RX STRAIN=BRISTOL N2;
RA Blini L., Heidt H., Liberatori S., Geter G., Pallini V., Zwilling R.;
RT "Two-dimensional gel electrophoresis of Caenorhabditis elegans
homogenates and identification of protein spots by microsequencing."
RL Electrophoresis 1:557-562(1997).
FT NON-TER 12 12
SQ SEQUENCE 12 AA; 1409 MW; 8DC4A7105316905A CRC64;

Query Match 40.0%; Score 14; DB 1; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DDL 6
Db 4 DDI 6

RESULT 13 UNO2_PINPS STANDARD; PRT; 13 AA.

ID UNO2_PINPS STANDARD; PRT; 13 AA.

AC P81667; 1:
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (N55) (FRAGMENTS).
OS Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC eudicotyledons; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
RN [1]
RP SEQUENCE.
RC TISSUE-NEEDLE;
RX MEDLINE: 99274088.
RA Costa P., Pionneau C., Bauw G., Dubois C., Bahrman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
proteins." (See http://www.isb-sib.ch/announce/
RL 20:1098-1108(1999).
CC -!- INDUCTION: BY WATER-STRESS.
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
CC PROTEIN IS: 5.4, ITS MW IS: 43 KD.
CC NON_TER 1 1
FT NON_CONS 7 8
FT NON_TER 13 13
SQ SEQUENCE 13 AA; 1559 MW; 966B5A43EF94B411 CRC64;

Query Match 40.0%; Score 14; DB 1; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TQDDL 6
Db 6 TRDNV 10

RESULT 14 RECJ_SALTY STANDARD; PRT; 14 AA.

ID RECJ_SALTY STANDARD; PRT; 14 AA.

AC P28355; 1:
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 01-FEB-1995 (Rel. 31, Last annotation update)
DE SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE RECJ (EC 3.1.1.-) (FRAGMENT).
GN RECJ.
OS Salmonella typhimurium;
OC Bacteria; proteobacteria;
RN [1]

RX	MEDLINE: 91046011;	DR	PROSITE: PS50059; FKBP_PPIASE_3; PARTIAL.
RA	Kawakami K., Nakamura Y.;	KW	Isomerase; Rotamase; Repeat; Calmodulin-binding.
RT	"Autogenous suppression of an opal mutation in the gene encoding	FT	1
RT	peptide chain release factor 2";	NON_TER	15
RT	Proc. Natl. Acad. Sci. U.S.A. 87: 8432-8436(1990).	FT	15
RL	-1- FUNCTION: SINGLE-STRANDED-DNA-SPECIFIC EXONUCLEASE. REQUIRED FOR	SEQUENCE	15 AA;
CC	MANY TYPES OF RECOMBINATIONAL EVENTS, ALTHOUGH THE STRINGENCY OF		1675 MW;
CC	THE REQUIREMENT FOR REC1 APPEARS TO VARY WITH THE TYPE OF		2B53999722277F3F CRC64;
CC	RECOMBINATIONAL EVENT MONITORED AND THE OTHER RECOMBINATION GENE		
CC	PRODUCTS WHICH ARE AVAILABLE.		
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	Query Match	40.0%; Score 14; DB 1; Length 15;
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -	Best Local Similarity	33.3%; Pred. No. 2.2e+03;
CC	the European Bioinformatics Institute. There are no restrictions on its	Matches	3; Mismatches 1; Indels 0; Gaps 0;
CC	use by non profit institutions as long as its content is in no way	Qy	2 TQDDLO 7
CC	modified and this statement is not removed. Usage by and for commercial	ID	FAR9_CALVO STANDARD;
CC	entities requires a license agreement. (See http://www.isb-sib.ch/announce/	AC	P41864;
CC	or send email to license@isb-sib.ch).	DB	10 TQDEVE 15
CC	-----	RESULT	16
CC	DRMBL: M38590; AAA72913; 1; -.	ID	FAR9_CALVO STANDARD;
DR	DRYNGENE; SG:0332; REC7.	AC	P41864;
Hydrolase; Nuclease; Exonuclease.	KW	DT	01-NOV-1995 (Rel. 32, Created)
NON_TER	1	DT	01-NOV-1995 (Rel. 32, Last sequence update)
SEQUENCE	14 AA; 1656 MW;	DI	01-NOV-1995 (Rel. 32, Last annotation update)
CC	105E784AC26C5650 CRC64;	DE	CALLIFMRFAIMIDE 9.
CC	-----	OS	Calliphora vomitoria (Blue blowfly).
DR	Eukaryote; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;	OC	Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
DR	Ostholioidea; Calliphoridae; Calliphora.	OC	
RP	SEQUENCE.	RN	[1]
RC	RC TISSUE: THORACIC GANGLION;	RP	
RC	RC MEDLINE: 9219611.	RX	
RA	Duwe H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,	RA	
RA	Rehfeld J.F., Thorpe A.;	RA	
RA	"Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2	RT	
RA	neuropeptides (designated callifmrfaimides) from the blowfly	RT	
AC	CALLIPHORA vomitoria."	RL	Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
AC	CC	CC	-I- SIMILARITY: BELONGS TO THE FAPP (FMRFAMIDE RELATED PEPTIDE)
AC	DR	DR	Family.
AC	DT	DT	I41978; I441978.
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	FT	Neuropeptide; Amidation.
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	MOD_RES	Calliphora vomitoria.
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	SEQUENCE	Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	Qy	2 TQDD 5
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	ID	LOSS_LOCMI STANDARD;
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	AC	P47733;
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	DT	01-FEB-1996 (Rel. 33, Created)
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	DT	01-FEB-1996 (Rel. 33, Last sequence update)
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	DT	15-DEC-1998 (Rel. 37, Last annotation update)
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	DE	SULFAKININ (LOM-5K).
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	OS	Locusta migratoria (Migratory locust).
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	OC	Eukaryote; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	OC	Pterygota; Neoptera; Orthopteroidea; Orthoptera; Caelifera;
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	OC	Acriodomorpha; Acridoidea; Acridoidea; Oedipodinae; Locusta.
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RN	[1]
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RP	SEQUENCE.
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RC	TISSUE-NEEDLE;
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RC	MEMLINE: 99274088.
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RA	Costa P., Plionneus C., Bauw G., Dubos C., Bahman N., Kremer A.,
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RA	"Genetic analysis of needle proteins in maritime pine. 1. Mapping
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RT	dominant and odontomin protein markers assayed on diploid tissue, in
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RT	a haploid-based genetic map";
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RT	Silvae Genetica 46:161-165(1997).
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RN	[2]
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RP	SEQUENCE.
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RC	TISSUE-BRAIN;
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RC	MEMLINE: 99274088.
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RA	Costa P., Plionneus C., Bauw G., Dubos C., Bahman N., Kremer A.,
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RA	"Separation and characterization of needle and xylem maritime pine
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RT	proteins";
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	RT	Electrophoresis 20:1098-1108(1999).
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	CC	-I- FUNCTION: PPIASE THAT BINDS CALMODULIN (BY SIMILARITY).
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	CC	-I- CATALYTIC ACTIVITY: PEPTIDYLPROLINE (OMEGA=180) =
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	CC	PEPTIDYLPROLINE (OMEGA=0).
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	CC	-I- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS PROTEIN IS:
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	CC	5.1, ITS MW IS: 72 KD.
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	CC	-I- SIMILARITY: BELONGS TO THE FKBP-TYPE PPIASE FAMILY.
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	DR	PROSITE: PS00453; FKBP_PPIASE_1; PARTIAL.
PKB7_PINS	PKB7_PINS STANDARD; PRT; 15 AA.	DR	PROSITE: PS00454; FKBP_PPIASE_2; PARTIAL.

RL PP.231-241, Plenum Press, New York (1990).
 CC -1- FUNCTION: MYOTROPIC PEPTIDE.
 CC -1- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR PROSIRE; PS00250; GASTRIN; 1.
 RW Hormone; Amidation; Sulfatation.
 FT MOD_RES 1 1 PYRROLIDONE CARBOXYLIC ACID.
 MOD_RES 7 7 SULFATATION (POTENTIAL).
 FT MOD_RES 12 AA; 1440 MW; 9B5B5D9BD65AAA CRC64;
 SQ SEQUENCE 12 AA; 12 AA; 1440 MW; 9B5B5D9BD65AAA CRC64;

Query Match 37.1%; Score 13; DB 1; Length 12;
 Best Local Similarity 40.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VTQDD 5
 Db 2 LASDD 6

RESULT 18
 UIAL_MOUSE STANDARD PRT; 12 AA.
 ID UIAL_MOUSE STANDARD PRT; 12 AA.
 AC P99032;_C
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF LIVER TISSUE (SPOT 2D-0014M9)
 DE (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Rodentia; Sciurognathli; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE.
 RC TISSUE-LIVER;
 RA Sanchez J.-C., Rouge V., Frutiger S., Hughes G.J., Yan J.X.,
 RA Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F.,
 RA Cowthorne M.;
 RL Submitted (AUG-1998) to the SWISS-PROT data bank.
 CC -1- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN
 CC PROTEIN IS: 5.0, ITS MW IS: 11.7 KD.
 DR SWISS-2DPAGE; P99032; MOUSE.
 FT NON-TER 12 12
 SQ SEQUENCE 12 AA; 1324 MW; DD6468EE9F75BAB6 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 12;
 Best Local Similarity 50.0%; Pred. No. 2.8e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 4 DPLQ 7
 Db 2 DNVQ 5

RESULT 19
 EP65_HUMAN STANDARD PRT; 13 AA.
 ID EP65_HUMAN STANDARD PRT; 13 AA.
 AC F54963;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE ERYTHROCYTE 65 KD PROTEIN (P65) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE, AND CARBOHYDRATE-BINDING SITE.
 RX MEDLINE; 90004678.
 RA Hart G.W., Haltianger R.S., Holt G.D., Kelly W.G.;
 RA "Nucleoplasmic and cytoplasmic glycoproteins.";
 RL Ciba Found. Symp. 145:102-118 (1989).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

RESULT 20
 LIGA_TRAVE STANDARD PRT; 13 AA.
 ID LIGA_TRAVE STANDARD PRT; 13 AA.
 AC P20011;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE LIGNINASE A (EC 1.11.1.-) (LIGNIN PEROXIDASE) (FRAGMENT).
 OS Trametes versicolor (White-rot fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Aphyllophorales;
 OC Coriolaceae; Trametes.
 RN [1]
 RP SEQUENCE.
 RA Joensson L., Karlsson O., Lundquist K., Nyman P.O.;
 RA "Trametes versicolor ligninase: isozyme sequence homology and
 substrate specificity,"
 RL FEBS Lett. 247:143-146 (1989).
 CC -1- CATALYTIC ACTIVITY: DEPOLYMERIZATION OF LIGNIN. CATALYSES THE
 CC (ALPHA)-C(BETA) CLEAVAGE OF THE PROPYL SIDE CHAINS OF LIGNIN.
 CC -1- PATHWAY: FIRST STEP IN LIGNIN DEGRADATION.
 DR PIR; S04013; S04013.
 DR PROSITE; PS00435; PROXIDASE_1; PARTIAL.
 DR PROSITE; PS0436; PROXIDASE_2; PARTIAL.
 DR Oxidoreductase; Peroxidase; Heme; Glycoprotein; Multigene family;
 KW Lignin degradation.
 FT NON-TER 13
 SQ SEQUENCE 13 AA; 1298 MW; 22C50ED5872A4338 CRC64;

Query Match 37.1%; Score 13; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 3e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTQDD 6
 Db 4 VSQPSL 9

RESULT 21
 LIGB_TRAVE STANDARD PRT; 13 AA.
 ID LIGB_TRAVE STANDARD PRT; 13 AA.
 AC P20012;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 01-FEB-1991 (Rel. 17, Last annotation update)
 DE LIGNINASE B (EC 1.11.1.-) (LIGNIN PEROXIDASE) (FRAGMENT).
 OS Trametes versicolor (White-rot fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Aphyllophorales;
 OC Coriolaceae; Trametes.
 RN [1]
 RP SEQUENCE.
 RX MEDLINE; 89211432.
 RA Joensson L., Karlsson O., Lundquist K., Nyman P.O.;
 RA "Trametes versicolor ligninase: isozyme sequence homology and
 substrate specificity,"
 RL FEBS Lett. 247:143-146 (1989).

CC -!- CATALYTIC ACTIVITY: DEPOLYMERIZATION OF LIGNIN. CATALYSES THE
CC C(ALPHA)-C(BETA) CLEAVAGE OF THE PROPYL SIDE CHAINS OF LIGNIN.
CC -!- PATHWAY: FIRST STEP IN LIGNIN DEGRADATION.
DR PIR: S04014; S04014.
DR PROSITE: PS00435; PEROXIDASE_1; PARTIAL.
DR PROSITE: PS00436; PEROXIDASE_2; PARTIAL.
KW Oxidoreductase; Peroxidase; Heme; Glycoprotein; Multigene family;
KW Lignin degradation; Non-TER 13 13 AA; 1269 MW; 22C50ED5B72A52C8 CRC64;
SQ SEQUENCE 13 AA; 1269 MW; 22C50ED5B72A52C8 CRC64;

Query Match Similarity 37.1%; Score 13; DB 1; Length 13;
Best Local Similarity 60.0%; Pred. No. 3e+03; 2; Indels 0; Gaps 0;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VTQDD 5
DR 1 RL30_SALTY STANDARD PRT; 13 AA.
Db 1 VTXPD 5

RESULT 22
RL30_SALTY STANDARD PRT; 13 AA.

DR 054-00; AC 15-DBC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
50S RIBOSOMAL PROTEIN L30 (FRAGMENT).
GN RPMD.
OS *Salmonella typhimurium*.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmoelida.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=L30;
RA Bjorkman J., Hughes D., Andersson D.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE L30 FAMILY OF RIBOSOMAL PROTEINS.

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or send an email to license@isb-sib.ch).

EMBL; A0223237; CAI1206.1; .
DR STYGENE; SG?????; RPMD.
DR PROSITE: PS00634; RIBOSOMAL_L30; PARTIAL.
KW Ribosomal protein.
FT INT-MER 0 0 BY SIMILARITY.
FT NON-TER 13 13 BY SIMILARITY.
SQ SEQUENCE 13 AA; 1431 MW; 15A0A8F886B3C1A0 CRC64;

Query Match Similarity 37.1%; Score 13; DB 1; Length 13;
Best Local Similarity 66.7%; Pred. No. 3e+03; 1; Mismatches 0; Indels 0; Gaps 0;
Matches 2; Conservative 2; Indels 0; Gaps 0;

Qy 1 VTQ 3
DR 6 RTQ 8

RESULT 23
HCVA_MEGCR STANDARD PRT; 14 AA.

DR Q10583; AC 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-FEB-2000 (Rel. 39, Last annotation update)

DE HEMOCYANIN A CHAIN (KLH-A) (FRAGMENT).
OS *Megathura crenulata*.
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Archaeogastropoda.
RN [1]
RP SEQUENCE.
RX MEDLINE: 96208935.
RA Swerdlow R.D.; Ebert R.F.; Lee P.; Bonaventura C.; Miller K.I.;
RT "Reyhole limpet hemocyanin: structural and functional
characterization of two different subunits and multimers.";
RL Comp. Biochem. Physiol. 118B:537-548(1996).
CC -!- FUNCTION: HEMOCYANIN ARE COPPER-CONTAINING OXYGEN CARRIERS
CC OCCURRING FREELY DISSOLVED IN THE HEMOLYMPH OF MANY MOLLUSKS AND
CC ARTHROPODS.
CC -!- SUBUNIT: DECAMERS AND DIDECAmers.
CC -!- SUBCELLULAR LOCATION: EXTRACELLULAR.
CC -!- TISSUE SPECIFICITY: HEMOLYMPH.
CC -!- SIMILARITY: BELONGS TO THE TYROSINASE FAMILY. HEMOCYANIN
CC SUBFAMILY.
DR PROSITE; PS00209; HEMOCYANIN_1; PARTIAL.
DR PROSITE; PS00210; HEMOCYANIN_2; PARTIAL.
KW Respiratory protein; Oxygen transport; Copper; Glycoprotein;
KW Hemolymph.
FT NON-TER 14 14 SEQUENCE 14 AA; 1610 MW; 9CE61977014A99D5 CRC64;
SQ Qy 1 VTQD 4
Db 11 LTAQE 14

RESULT 24
ITRB_ALBUJU STANDARD PRT; 15 AA.
ID ITRB_ALBUJU
AC P24927;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE TRYPSIN INHIBITOR B CHAIN (FRAGMENT).
OS *Albulia julibrissin* (Silk tree).
OC Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC euphyllophytes; Spermatophyta; Magnoliophyta; Eudicotyledons;
OC core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Mimosoideae;
OC Albulia.
RN [1]
RP SEQUENCE.
RC TISSUE=SEED;
RX MEDLINE: 80115605.
RA Odani S., Ono T.; Ikenaka T.;
RT "Proteinase inhibitors from a mimosoideae legume, *Albizia julibrissin*. Homologues of soybean trypsin inhibitor (Kunitz)." ;
RL J. Biochem. 86:1795-1805(1979).
CC -!- FUNCTION: INHIBITS TRYPSIN AND ALPHA-CHYMOTRYPSIN.
CC -!- SUBUNIT: HETERO-DIMER OF AN "A" AND A "B" CHAIN LINKED BY A
CC DISULFIDE BOND.
CC -!- SIMILARITY: TO BETA CHAINS OF SOME OTHER LEGUMINOUS KUNITZ-TYPE
CC INHIBITORS.
KW Serine protease inhibitor.
FT NON-TER 15 15 SEQUENCE 15 AA; 1705 MW; 53165F7E9C45B4D0 CRC64;
SQ Qy 3 QDD 5

Query Match Similarity 37.1%; Score 13; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 3e+03; 1; Mismatches 0; Indels 0; Gaps 0;

Db 1 KDD 3

RESULT 25
ID RKG_CARCR STANDARD; PRT; 15 AA.
AC P21586;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-AUG-1991 (Rel. 18, Last sequence update)
DE RATHKE'S GLAND GLYCOPROTEIN (FRAGMENT).
OS Caretta, caretta (Loggerhead).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Testudines;
OC Cryptodira; Chelonioidea; Cheloniidae; Caretta.
RN [1]
RP SEQUENCE.
RX TISSUE=RATHKE'S GLAND;
MEDLINE; 90075703.
RA Radhakrishna G., Chin C.Q., Wold F., Weldon P.J.;
RT Glycoproteins in Rathke's gland secretions of loggerhead (Caretta
caretta) and Kemp's Ridley (Lepidochelys kempi) sea turtles. ";
RL Comp. Biochem. Physiol. 98B:375-378(1989).
CC -!- FUNCTION: RATHKE'S GLAND SECRETIONS MAY FUNCTION AS PHEROMONES,
AS PREDATOR REPELLENTS, OR CONTRIBUTE TO THE MAINTENANCE OF THE
TURTLE SHELL.
CC -!- SIMILARITY: WITH RATHKE'S GLAND GLYCOPROTEIN FROM KEMP'S RIDLEY
SPA TURTLE.
DR PIR: PL0154; PL0154.
KW GLycoprotein.
FT NON_TER 15 15 MW; CC893BAAA1B1B5ED CRC64;
SQ SEQUENCE 15 AA; 1477 MW;

Query Match Score 13; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 TODD 5
Db 1 SDDD 4

RESULT 26
ID UN01_P1NPS STANDARD; PRT; 15 AA.
AC P81106;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DE UNKNOWN PROTEIN FROM 2D-PAGE OF NEEDLES (S1247/S1248) (N150/N151)
DE (FRAGMENT).
OS Pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophytina; Embryophytina; Tracheophytina;
OC euphylllophytes; Spermatophytina; Coniferopsida; Coniferales; Pinaceae;
OC Pinus.
RN [1]
RP SEQUENCE.
RC TISSUE-NEEDLE;
RA Plomion C., Costa P., Bahman N., Frigerio J.M.;
RT "Genetic analysis of needle proteins in maritime pine. 1. Mapping
dominant and codominant protein markers assayed on diploid tissue, in
a haploid-based genetic map.";
RU Silvae Genetica 46:161-165(1997).
RN [2]
RP SEQUENCE.
RC TISSUE-NEEDLE;
MEDLINE; 99274088.
RA Costa P., Pilonneau C., Bauw G., Dubos C., Bahman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT Separation and characterization of needle and xylem maritime pine
proteins.";
RU Electrophoresis 20:1098-1108(1999).
CC -!- MISCELLANEOUS: ON THE 2D-GEL THE DETERMINED PI OF THIS UNKNOWN

CC PROTEIN IS: 5.5, ITS MW IS: 62 KD.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1670 MW; 29CE44CD51E98FCF CRC64;

Query Match Score 13; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 3.5e+03;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTQ 3
Db 5 ITQ 7

RESULT 27
ID PAR2_CALVO STANDARD; PRT; 9 AA.
AC P41857;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE CALIFMRFAMIDE 2.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Oestrioidae; Calliphoridae; Calliphora.
RN [1]
RP SEQUENCE.
RC TISSUE=THORACIC GANGLION;
MEDLINE; 92196111.
RA Rehfeld J.F., Thorpe A.;
RA Dube H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,
RN Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH2
neuropeptides (designated callifMRFamides) from the blowfly
Calliphora vomitoria;"
RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
CC -!- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
CC SALIVARY GLAND OF CALLIPHORA.
CC -!- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
CC FAMILY.
DR PIR: B41978; B41978.
KW Neuropeptide; Amidation.
FT MOD_RES 9 9 AMIDATION.
SQ SEQUENCE 9 AA; 1128 MW; 29D0069CABBC5A7 CRC64;

Query Match Score 12; DB 1; Length 9;
Best Local Similarity 66.7%; Pred. No. 8.4e+04;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 TQD 4
Db 3 SQD 5

RESULT 28
ID PAR3_CALVO STANDARD; PRT; 9 AA.
AC P41858;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE CALIFMRFAMIDE 3.
OS Calliphora vomitoria (Blue blowfly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
RN [1]
RP SEQUENCE.
RC TISSUE=THORACIC GANGLION;
MEDLINE; 92196111.
RA Dube H., Johnsen A.H., Sewell J.C., Scott A.G., Orchard I.,

RA Rehfeld J.F.; Thorpe A.;
 RT "Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH₂
 RT neuropeptides (designated calliphorafanides) from the blowfly
 Calliphora vomitoria.";
 RL Proc. Natl. Acad. Sci. U.S.A. 89:2326-2330(1992).
 CC -I- FUNCTION: ABLE TO INDUCE FLUID SECRETION FROM THE ISOLATED
 SALIVARY GLAND OF CALLIPHORA.
 CC -I- SIMILARITY: BELONGS TO THE FARP (FMRFAMIDE RELATED PEPTIDE)
 FAMILY.
 CC PIR: C41978; C41978.
 KW Neuropeptide; Amidation.
 FT MOD_RES 9 9
 SEQUENCE 9 AA; 1114 MW; 2F0B0699CAB6C5A7 CRC64;

Query Match 29
 Best Local Similarity 34.3%; Score 12; DB 1; Length 9;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Qy 2 TQD 4
 :|:
 Db 3 SQD 5

RESULT 29
 NSR1_SARBU STANDARD; PRT; 9 AA.
 AC P41492;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE NEOSULFARKININ-I (NEB-SK-I).
 OS Sarcophaga bullata (Grey flesh fly) (Neobellertia bullata).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Oestroidea; Sarcophagidae; Sarcophaga.
 [1]
 RN
 RP
 SEQUENCE.
 RC TISSUE-HEAD.
 RX MEDLINE:93083101.
 RA Fonagy A.; Schools L.; Proost P.; van Damme J.; de Loof A.;
 RT "Isolation and primary structure of two sulfakinin-like peptides from
 the fleshfly, Neobellertia bullata.";
 RL Comp. Biochem. Physiol. 101C:135-142(1992).
 CC -I- FUNCTION: MYONROPIC PEPTIDE.
 CC -I- SIMILARITY: BELONGS TO THE GASTRIN/CHOLECYSTOKININ FAMILY.
 DR PROTEIN:PS00259; GASTRIN; 1.
 KW Neuropeptide; Amidation; Sulfatation.
 FT MOD_RES 4 4
 FT MOD_RES 9 9
 SEQUENCE 9 AA; 1187 MW; 8B0B0691B65RA CRC64;

Query Match 30
 Best Local Similarity 34.3%; Score 12; DB 1; Length 9;
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 4 DD 5
 :|:
 Db 2 DD 3

RESULT 30
 UHA2_HUMAN STANDARD; PRT; 9 AA.
 ID UHA2_HUMAN
 AC P40929;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DE UNKNOWN PROTEIN FROM 2D-PAGE OF HEART (SPOT 5603) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Primates; Catarrhini; Hominidae; Homo.

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OM protein - protein search, using sw model

Run on: June 30, 2000, 14:07:09 ; Search time 53.11 Seconds

(without alignments)
9.138 Million cell updates/secTitle: US-08-833-506C-89
Perfect score: 35
Sequence: 1 vTQDDLQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 225878 seqs, 69334122 residues

Total number of hits satisfying chosen parameters: 1120

Minimum DB seq length: 0

Maximum DB seq length: 15

Post-processing: Minimum Match %

Listing first 100 summaries

Database : SPTRIMBL_12:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_rhodent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.

Score

Query

Match

Length

DB

ID

Description

1	20	57.1	12	4	Q13695	Q13695 homo sapien
2	20	57.1	14	12	Q84179	Q4179 porcine ade
3	19	54.3	11	9	Q3815	P3415 bacterioph
4	17	48.6	12	8	P92457	epheda sp.
5	17	48.6	15	2	Q53541	P5541 bacillus sp.
6	15	42.9	8	4	Q15893	Q15893 homo sapien
7	15	42.9	9	11	Q63924	Q63924 mus musculu
8	15	42.9	11	2	Q47602	Q47602 escherichia
9	15	42.9	14	11	Q921H4	Q921H4 mus musculu
10	15	42.9	15	4	Q08947	Q08947 homo sapien
11	15	42.9	15	4	Q16387	Q16387 homo sapien
12	14	40.0	8	2	P72279	P72279 rhodococcus
13	14	40.0	8	4	Q15902	Q15902 homo sapien
14	14	40.0	8	5	Q94695	Q94695 physarum po
15	14	40.0	11	2	Q23876	Q23876 dictyosteli
16	14	40.0	13	2	Q48357	Q48357 escherichia
17	14	40.0	13	5	Q61340	Q61340 paenilirius 1
18	14	40.0	14	4	Q16118	Q16118 homo sapien
19	14	40.0	14	12	P91578	P91578 choristoneu
20	14	40.0	15	15	P52640	P52640 pseudomonas

21	13	37.1	13	37.1	Q47556	Q47556 escherichia
22	13	37.1	10	11	Q83622	Q83622 murray vall
23	13	37.1	11	4	Q63056	Q63056 rattus norv
24	13	37.1	11	4	Q16427	Q16427 homo sapien
25	13	37.1	11	7	Q78119	Q78119 oreochromis
26	13	37.1	12	8	Q36622	Q36622 picea abies
27	13	37.1	12	8	Q36623	Q36623 picea abies
28	13	37.1	12	8	Q36668	Q36668 pinus sylve
29	13	37.1	12	8	Q36669	Q36669 pinus sylve
30	13	37.1	12	8	Q37791	Q37791 larix euro
31	13	37.1	12	8	Q37790	Q37790 larix euro
32	13	37.1	12	8	Q03815	Q03815 abies alba
33	13	37.1	12	8	Q03816	Q03816 metasequoia
34	13	37.1	14	2	Q92460	Q92460 taxus bacca
35	13	37.1	14	2	Q92442	Q92442 streptococc
36	13	37.1	15	10	Q08936	Q08936 nicotiana t
37	13	37.1	15	12	Q97090	Q97090 human immun
38	13	37.1	15	13	Q90403	Q90403 discopyge o
39	12	34.3	7	2	Q5448	Q5448 streptomyce
40	12	34.3	7	10	Q49223	Q49223 glycine max
41	12	34.3	9	12	Q70140	Q70140 human immun
42	12	34.3	10	2	P96105	P96105 alteromonas
43	12	34.3	10	10	Q08938	Q08938 pseudomonas
44	12	34.3	11	2	Q52326	Q52326 plasmid sym
45	12	34.3	13	4	Q14461	Q14461 homo sapien
46	12	34.3	13	4	Q93674	Q93674 homo sapien
47	12	34.3	13	11	Q63047	Q63047 rattus norv
48	12	34.3	13	11	Q62093	Q62093 pigeon pea
49	12	34.3	14	2	P78359	P78359 homo sapien
50	12	34.3	14	4	P78359	P78359 homo sapien
51	12	34.3	14	4	Q16232	Q16232 homo sapien
52	12	34.3	14	5	Q26100	Q26100 pratylenchu
53	12	34.3	14	12	Q66201	Q66201 porcine tra
54	12	34.3	15	2	Q68430	Q68430 buchnera ap
55	12	34.3	15	2	Q54325	Q54325 staphylococ
56	12	34.3	15	10	Q40562	Q40562 nicotiana t
57	12	34.3	15	10	Q40563	Q40563 nicotiana t
58	12	34.3	15	11	Q9203	Q9203 rattus norv
59	12	34.3	15	12	Q97092	Q97092 human immun
60	12	34.3	15	12	Q97094	Q97094 human immun
61	11	31.4	8	2	Q921E9	Q921E9 neisseria m
62	11	31.4	9	12	Q85710	Q85710 rous sarcom
63	11	31.4	10	4	Q60912	Q60912 homo sapien
64	11	31.4	10	12	Q86580	Q86580 simian para
65	11	31.4	11	2	Q47600	Q47600 escherichia
66	11	31.4	11	2	Q47614	Q47614 escherichia
67	11	31.4	11	2	Q47569	Q47569 escherichia
68	11	31.4	11	12	P88018	P88018 human immun
69	11	31.4	11	13	Q90735	Q90735 gallus gall
70	11	31.4	13	2	Q50038	Q50038 mycobacteri
71	11	31.4	13	2	Q47501	Q47501 escherichia
72	11	31.4	13	4	Q15537	Q15537 homo sapien
73	11	31.4	13	5	Q24165	Q24165 drosophila
74	11	31.4	13	5	Q9X42	Q9X42 albinaria h
75	11	31.4	13	11	Q60517	Q60517 mus musculu
76	11	31.4	13	12	Q61219	Q61219 vesicular s
77	11	31.4	14	2	Q9Z1E1	Q9Z1E1 acetobacter
78	11	31.4	14	2	Q52840	Q52840 rhizobium l
79	11	31.4	14	2	Q9X715	Q9X715 campylobact
80	11	31.4	14	2	Q9W79	Q9W79 campylobact
81	11	31.4	14	12	Q84708	Q84708 porcine epi
82	11	31.4	15	2	Q54398	Q54398 salmonella
83	11	31.4	15	2	Q47892	Q47892 fremyella d
84	11	31.4	15	6	Q46661	Q46661 macropus ro
85	10	28.6	7	11	Q07354	Q07354 synchococc
86	10	28.6	7	11	Q63480	Q63480 rattus norv
87	10	28.6	8	2	Q68485	Q68485 klebsiella
88	10	28.6	8	4	Q15895	Q15895 homo sapien
89	10	28.6	8	5	Q15899	Q15899 babeia ovi
90	10	28.6	8	7	Q29880	Q29880 homo sapien
91	10	28.6	8	11	Q61715	Q61715 mus musculu
92	10	28.6	8	12	Q66807	Q66807 echovirus 2
93	10	28.6	9	2	Q45533	Q45533 bacillus su

RESULT 1
 Q1395 PRELIMINARY; PRT; 12 AA.
 AC Q1395;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE ACETYLCHOLINE RECEPTOR (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=THYMUS;
 RX MEDLINE: 94071933.
 RA MIROVILOVIC M.; MAT Y.; HERBSTREITH M.; RUBBOLI F.; TARRONI P.,
 CLEMENTI F.; ROSES A.D.;
 RT "Splicing of an anti-sense Alu sequence generates a coding sequence
 variant for the alpha-3 subunit of a neuronal acetylcholine
 receptor";
 RL Biochem. Biophys. Res. Commun. 197:137-144 (1993);
 EMBL: L18973; AAAA6792.1; -.
 FT NON-TER 1 1
 SEQUENCE 12 AA; 1282 MW; CF969363 CRC32;

Query Match 57.1%; Score 20; DB 4; Length 12;
 Best Local Similarity 57.1%; Pred. No. 2.5e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VTODDLQ 7
 Db 6 VTONGVQ 12

RESULT 2
 Q84179 PRELIMINARY; PRT; 14 AA.
 AC Q84179;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1996 (TREMBLrel. 01, Last annotation update)
 DE PROTEINASE (FRAGMENT).
 GN 23K.
 OS Porcine adenovirus 3.
 OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MCCOY R.J.; JOHNSON M.A.; SHEPPARD M.;
 RL Submitted (AUG-1993) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; U45921; AAB02184.1; -.
 FT NON-TER 14 14
 SEQUENCE 14 AA; 1582 MW; 478FF81D CRC32;

Query Match 57.1%; Score 20; DB 12; Length 14;
 Best Local Similarity 50.0%; Pred. No. 3e+02; Indels 0; Gaps 0;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VTODDLQ 7
 I:::|:

RESULT 3
 Q38415 PRELIMINARY; PRT; 11 AA.
 AC Q38415;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DE ANTI PROTEIN (FRAGMENT).
 OS Bacteriophage P7.
 OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 90335968.
 RA CITRON M.; SCHUSTER H.;
 RT "The c4 repressors of bacteriophages P1 and P7 are antisense RNAs.";
 RL Cell 62:591-598(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92319637.
 RA CITRON M.; SCHUSTER H.;
 RT RNA.";
 RL Nucleic Acids Res. 20:3085-3090(1992).
 DR EMBL; M35139; AAA32437.1; -.
 FT NON-TER 11 11
 SQ SEQUENCE 11 AA; 1315 MW; F2E5018A CRC32;

Query Match 54.3%; Score 19; DB 9; Length 11;
 Best Local Similarity 50.0%; Pred. No. 3.7e+02; Indels 0; Gaps 0;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VTODDL 6
 I:::|:
 Db 6 VTRNDI 11

RESULT 4
 P92457 PRELIMINARY; PRT; 12 AA.
 AC P92457;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE CHLOROPLAST SUBUNIT OF LIGHT-INDEPENDENT PROTOCHLOROPHYLLIDE
 REDUCTASE (FRAGMENT).
 GN CHLB GENE.
 OS Chloroplast.
 OG Eukaryota; Viridiplantae; Streptophytta; Embryophytta;
 OC euphyllophytes; Spermatophytta; Gnetophytta; Ephedrales;
 OC Ephedraceae; Ephedra.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 97263785.
 RA KARPINSKA B.; KARPINSKI S.; HALLIGREN J.E.;
 RT The chlb gene encoding a subunit of light-independent
 protoclorophyllide reductase is edited in chloroplasts of conifers.";
 RL Curr. Genet. 31:343-347(1997).
 DR EMBL; X98573; CAR67182.1; -.
 KW Chloroplast.
 FT NON-TER 1 1
 SQ SEQUENCE 12 AA; 1441 MW; B036E488 CRC32;

Query Match 48.6%; Score 17; DB 8; Length 12;
 Best Local Similarity 75.0%; Pred. No. 1.1e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VTODDLQ 7
 I:::|:

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 8801493.
 RX TSUGE I., SHEN F., W.W. STEINMETZ M., BOYSE E.A.;
 "A gene in the H-2S:H-2D interval of the major histocompatibility
 complex which is transcribed in B cells and macrophages.";
 RL Immunogenetics 26:378-380(1987).
 DR EMBL: M18187; AAA57272.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 14 AA; 1542 MW; 607F3593 CRC32;
 Qy 5 DLQ 7
 Db 3 DLQ 5
 Query Match 42.9%; Score 15; DB 11; Length 14;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;
 Qy 10
 ID Q08947 PRELIMINARY; PRT; 15 AA.
 AC Q08947; PRELIMINARY;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE DYSTROPHIN (DP121.6) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo; Homo.
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 93291881.
 RA BYERS T.J., LIDOV H.G., KUNKEEL L.M.;
 RT "An alternative dystrophin transcript specific to peripheral nerve."
 RL Nat. Genet. 4:77-81(1993).
 DR EMBL: S62617; AAB27159.1; -.
 KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
 KW Duplication; Alternative splicing.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1855 MW; AE9F9478 CRC32;
 Qy 5 DLQ 7
 Db 11 DLQ 13
 Query Match 42.9%; Score 15; DB 4; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 0; Mismatches 0;
 Qy 11
 ID Q16387 PRELIMINARY; PRT; 15 AA.
 AC Q16387; PRELIMINARY;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DT 01-NOV-1999 (TREMBLrel. 12, Last annotation update)
 DE MEX40 PROTEIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 Eutheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 95400293.
 RX BUDARF M.L., COLLINS J., GONG W., ROE B., WANG Z., BAILEY L.C.,
 RA SPILLINGER B., MICHAUD D., DRISCOLL D.A., EMANUEL B.S.;
 RA RT "Cloning a balanced translocation associated with DiGeorge syndrome
 and identification of a disrupted candidate gene.";
 RL Nat. Genet. 10:269-270(1995).
 DR EMBL: S79494; AAD14301.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 15 AA; 1626 MW; 746EE62B CRC32;
 Qy 3 QDDLQ 7
 Db 10 RDGLQ 14
 Query Match 42.9%; Score 15; DB 4; Length 15;
 Best Local Similarity 60.0%; Pred. No. 3.e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 12
 ID P72279 PRELIMINARY; PRT; 8 AA.
 AC P72279; PRELIMINARY; PRT; 8 AA.
 DT 01-FEB-1997 (TREMBLrel. 02, Created)
 DT 01-FEB-1997 (TREMBLrel. 02, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE BI-PHENYL DIOXYGENASE (FRAGMENT).
 RN GN
 RP SEQUENCE FROM N.A.
 RX BPHB.
 RA Rhodococcus globuberulus.
 OC ASTURIAS J.A., DIAZ E., TIMMIS K.N.;
 OC Bacteria; Firmicutes; Actinobacteria; Actinomycetales; Rhodococcus.
 OC Actinomycetales; Corynebacterineae; Nocardiaceae; Rhodococcus.
 RN [1]
 RN DE
 RN SEQUENCE FROM N.A.
 RX Rhodococcus globuberulus.
 RA ASTURIAS J.A., DIAZ E., TIMMIS K.N.;
 RT "The evolutionary relationship of biphenyl dioxygenase from gram-
 positive Rhodococcus globuberulus P6 to multicomponent dioxygenases from
 gram-negative bacteria.";
 RT Gene 156:11-18(1995).
 RL RN
 KW RDXLINE; 95355652.
 DR X8004.; CAAS56350.1; -.
 FT NON_TER 8 8
 SQ SEQUENCE 8 AA; 989 MW; ED28AD0A CRC32;
 Qy 13
 ID Q15902 PRELIMINARY; PRT; 8 AA.
 AC Q15902; PRELIMINARY; PRT; 8 AA.
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE (CLONE XP7ETA) (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Butheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RA LEE C.C., YAZDANI A., WEHNERT M., BAILEY J., COUCH L., XIONG M.,
 RA COOLBAUGH M.I., CHINNULT C.A., BALDINI A., LINDSAY E.A., ZHAO Z.Y.,
 RA CASKEY C.T.H.;
 RL Hum. Mol. Genet. 0:0-0(0).
 DR EMBL: L32081; AAA73892.1; -.
 FT NON_TER 1 1

NON-TER	SEQUENCE	8	AA;	931	MW;	4RCB6ACD CRC32;	Db	4	EDVQ	7
NON-TER	8 AA;	931	MW;	4RCB6ACD CRC32;						
Query Match	Best Local Similarity	40.0%		Score 14;	DB 4;	Length 8;	RESULT	16		
Matches	3; Conservative	75.0%		Pred. No.	2.3e+05;		ID	Q48357	PRELIMINARY;	
	0; Mismatches	0;		Indels	0;	Gaps 0;	ID	Q48357;	PRT;	13 AA.
QY	1	VTDQ	4				AC	Q48357;		
	2	VTD	5				DT	01-NOV-1996	(TREMBLrel. 01, Created)	
Db							DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
							DT	01-NOV-1998	(TREMBLrel. 08, Last annotation update)	
							DE		TRANSCRIPTION TERMINATION FACTOR RHO (FRAGMENT).	
							GN		RHO.	
							OS		Escherichia coli.	
							OC		Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	
							OC		Escherichia.	
RESULT	14						RN	[1]		
	Q94695						RP		SEQUENCE FROM N.A.	
ID	Q94695;						RX		MEDLINE; 95139907.	
AC	01-FEB-1997	(TREMBLrel.	02,				RA		OPPERMAN T., MARTINEZ A., RICHARDSON J.P.;	
DT	01-FEB-1997	(TREMBLrel.	02,				RT		"The ts15 mutation of Escherichia coli alters the sequence of the C-	
DT	01-NOV-1998	(TREMBLrel.	08,				RT		terminal nine residues of Rho protein."	
DE							RL		Gene 152:133-134 (1995).	
GN							DR		EMBL: L34404; AAA8985.1;	
OS							FT		Transcription termination.	
Physarum polycephalum (Slime mold).							NON-TER	1	-	
Eukaryota; Myxogastria; Physarida; Physarum.							SEQUENCE	13 AA;	1531 MW;	43726F49 CRC32;
[1]										
SEQUENCE FROM N.A.										
RX										
MEDLINE; 96182101.										
RA										
BENARD M., LAGNEL C., PAILLOTA D., PIERRON G.;										
"Mapping of a replication origin within the promoter region of two										
unlinked, abundantly transcribed actin genes of Physarum										
polycephalum."										
RT										
Mol. Cell. Biol. 16:968-976 (1996).										
EMBL: M73459; AAB03706.1; -.										
DR										
MT	8		8							
NON-TER	8 AA;	878	MW;	6204C0E2 CRC32;						
SEQUENCE										
NON-TER										
RESULT	14									
	Q94695									
ID	Q94695;									
AC	01-FEB-1997	(TREMBLrel.	02,							
DT	01-FEB-1997	(TREMBLrel.	02,							
DT	01-NOV-1998	(TREMBLrel.	08,							
DE										
GN										
SHAKER.										
OS										
Patulirus interruptus (California spiny lobster).										
OC										
Eubaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;										
OC										
Eumalacostraca; Eucaria; Decapoda; Palinura;										
Palinuridae; Palinurus.										
RN										
RESULT	17									
	Q61340									
ID	Q61340;									
AC	061340;									
DT	01-AUG-1998	(TREMBLrel.	07,							
DT	01-AUG-1998	(TREMBLrel.	07,							
DE										
PONASUM CHANNEL (FRAGMENT).										
GN										
SHAKER.										
OS										
Patulirus interruptus (California spiny lobster).										
OC										
Eubaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;										
OC										
Eumalacostraca; Eucaria; Decapoda; Palinura;										
Palinuridae; Palinurus.										
RN										
RESULT	17									
	Q61340									
ID	Q61340;									
AC	061340;									
DT	01-AUG-1998	(TREMBLrel.	07,							
DT	01-AUG-1998	(TREMBLrel.	07,							
DE										
PONASUM CHANNEL (FRAGMENT).										
GN										
SHAKER.										
OS										
Patulirus interruptus (California spiny lobster).										
OC										
Eubaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;										
OC										
Eumalacostraca; Eucaria; Decapoda; Palinura;										
Palinuridae; Palinurus.										
RN										
RESULT	17									
	Q61340									
ID	Q61340;									
AC	061340;									
DT	01-AUG-1998	(TREMBLrel.	07,							
DT	01-AUG-1998	(TREMBLrel.	07,							
DE										
PONASUM CHANNEL (FRAGMENT).										
GN										
SHAKER.										
OS										
Patulirus interruptus (California spiny lobster).										
OC										
Eubaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;										
OC										
Eumalacostraca; Eucaria; Decapoda; Palinura;										
Palinuridae; Palinurus.										
RN										
RESULT	18									
	Q16118									
ID	Q16118									
AC	Q16118									
DT	01-NOV-1996	(TREMBLrel.	01,							
DT	01-NOV-1996	(TREMBLrel.	01,							
DE										
FARNHAM J. ,										
HARRIS WARRICK R.M.;										
DR										
RL										
Recept. Channels 00-011998).										
KW										
Ionic channel.										
FT										
NON-TER	13									
SEQUENCE	13 AA;	1336	MW;	5B640D04 CRC32;						
NON-TER										
RESULT	18									
	Q16118									
ID	Q16118									
AC	Q16118									
DT	01-NOV-1996	(TREMBLrel.	01,							
DT	01-NOV-1996	(TREMBLrel.	01,							
DE										
COLD HARV. SYMP. BIOL.										
EMBL: K02957; AAA33150.1; -.										
EMBL: K02956; AAA33150.1; JOINED.										
SEQUENCE 11 AA;	1205	MW;	0F2D057D CRC32;							
NON-TER										
RESULT	18									
	Q16118									
ID	Q16118									
AC	Q16118									
DT	01-NOV-1996	(TREMBLrel.	01,							
DT	01-NOV-1996	(TREMBLrel.	01,							
DE										
COLD HARV. SYMP. BIOL.										
EMBL: K02957; AAA33150.1; -.										
EMBL: K02956; AAA33150.1; JOINED.										
SEQUENCE 11 AA;	1205	MW;	0F2D057D CRC32;							
NON-TER										
RESULT	18									
	Q16118									
ID	Q16118									
AC	Q16118									
DT	01-NOV-1996	(TREMBLrel.	01,							
DT	01-NOV-1996	(TREMBLrel.	01,							
DE										
COLD HARV. SYMP. BIOL.										
EMBL: K02957; AAA33150.1; -.										
EMBL: K02956; AAA33150.1; JOINED.										
SEQUENCE 11 AA;	1205	MW;	0F2D057D CRC32;							
NON-TER										
RESULT	18									
	Q16118									
ID	Q16118									
AC	Q16118									
DT	01-NOV-1996	(TREMBLrel.	01,							
DT	01-NOV-1996	(TREMBLrel.	01,							
DE										
COLD HARV. SYMP. BIOL.										
EMBL: K02957; AAA33150.1; -.										
EMBL: K02956; AAA33150.1; JOINED.										
SEQUENCE 11 AA;	1205	MW;	0F2D057D CRC32;							
NON-TER										
RESULT	18									
	Q16118									
ID	Q16118									
AC	Q16118									
DT	01-NOV-1996	(TREMBLrel.	01,							
DT	01-NOV-1996	(TREMBLrel.	01,							
DE										
COLD HARV. SYMP. BIOL.										
EMBL: K02957; AAA33150.1; -.										
EMBL: K02956; AAA33150.1; JOINED.										
SEQUENCE 11 AA;	1205	MW;	0F2D057D CRC32;							
NON-TER										
RESULT	18									
	Q16118									
ID	Q16118									
AC	Q16118									
DT	01-NOV-1996	(TREMBLrel.	01,							
DT	01-NOV-1996	(TREMBLrel.	01,							
DE										
COLD HARV. SYMP. BIOL.										
EMBL: K02957; AAA33150.1; -.										
EMBL: K02956; AAA33150.1; JOINED.										

AC Q16118;	DT 01-NOV-1996 (TREMBLrel. 01, Created)	OC Bacteria; Proteobacteria.
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	RN [1]	RN SEQUENCE FROM N.A.
DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)	RC STRAIN=NTW3;	RC MEDLINE; 98215169.
DE CYCLIC ADENOSINE 3',5'-MONOPHOSPHATE RESPONSE ELEMENT BINDING PROTEIN	RA JAMES K.D., WILLIAMS P.A.;	RT "ntn" genes determining the early steps in the divergent catabolism of 4-nitrotoluene and toluene in <i>Pseudomonas</i> sp. strain TW3.;"
OS CREB (ALTERNATIVELY SPLICED, EXON W) (FRAGMENT).	RT RL J. Bacteriol. 180:2043-2049(1998).	RT DR EMBL; AF043544; AAC38356.1; -.
OC Homo sapiens (Human).	FT NON-TER 1	FT NON-TER 1
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;	SEQUENCE 15 AA; 1781 MW; FDD1B267 CRC32;	SEQUENCE 15 AA; 1781 MW; FDD1B267 CRC32;
PRIMATES; Catarrhini; Hominoidea; Homo.		
RN [1]		
SEQUENCE FROM N.A.		
RX MEDLINE; 94158910		
RA WEBER G., MEYER T.E., LESTEUR M., HERMANN H.L., GERARD N.,		
RA HABENER J.H.;		
RA [1]		
RT Developmental stage-specific expression of cyclic adenosine 3',5'-monophosphate response element binding protein CREB during spermatogenesis involves alternative exon splicing.;"		
RT Mol. Endocrinol. 7:1501-1501(1993).		
RL EMBL; S68577; AAC29985.1; -.		
DR FT NON-TER 1		
SEQUENCE 14 AA; 1698 MW; 86068950 CRC32;		
Query Match 40.0%; Score 14; DB 4; Length 14;	RESULT 21	Query Match 40.0%; Score 14; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 5.6e+03;	Q47556	Best Local Similarity 60.0%; Pred. No. 6e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	ID Q47556	Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
	PRELIMINARY;	
Qy 1 VTQD 4	AC AC	Qy 3 QDDLQ 7
Db 5 VQD 8	DT DT	Db 8 QSQLQ 12
	DT 01-NOV-1996 (TREMBLrel. 01, Created)	
	DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)	
	DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)	
	DE DE ASPARTATE TRANSCARBAMOYLASE REGULATORY CHAIN (FRAGMENT).	
	GN GN PYR1.	
	OS OS Escherichia coli.	
	OC OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	
	OC OC Escherichia.	
	RN [1]	
	AC AC	
	P11578; PRELIMINARY;	
	P11578; PRELIMINARY;	PRT; 14 AA.
	DT 01-MAY-1997 (TREMBLrel. 03, Created)	
	DT 01-AUG-1997 (TREMBLrel. 03, Last sequence update)	
	DT 01-AUG-1998 (TREMBLrel. 07, Last annotation update)	
	DE NUCLEOSIDE TRIPHOSPHATE PHOSPHOHYDROLASE (FRAGMENT).	
	GN NP_1.	
	OS Choristoneura fumiferana entomopoxvirus (CIEPV).	
	OC viruses; dsDNA viruses, no RNA stage: Poxviridae; Entomopoxvirinae;	
	OC Entomopoxvirus B.	
	RN [1]	
	RP RP SEQUENCE FROM N.A.	
	RA RA HOOVER T.A., ROOF W.D., FOLTERMANN K.F., O'DONOVAN G.A., BENCINI D.A.,	
	RA RA WILD J.R.;	
	RA RA PAUZA C.D., KARELS M.J., NAVRE M., SCHACHMAN H.K.;	
	RT RT "Genes encoding Escherichia coli aspartate transcarbamoylase: the pyrB-pyrI operon."	
	RT RT Proc. Natl. Acad. Sci. U.S.A. 79:4020-4024 (1982).	
	RN RN [2]	
	RP RP SEQUENCE OF 1-5 FROM N.A.	
	RA RA MEDLINE; 83195078.	
	RA RA LI X., BARRETT J.W., YUEN L., ARIF B.M.;	
	RA RA DR DR Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.	
	RA RA DR DR EMBL; U19239; AAC39411.1; -.	
	KW KW Hydrolase.	
	FT FT NON-TER 1	
	SEQUENCE 14 AA; 1762 MW; 940E3C99 CRC32;	
	Query Match 40.0%; Score 14; DB 12; Length 14;	Query Match 37.1%; Score 13; DB 2; Length 9;
	Best Local Similarity 50.0%; Pred. No. 5.6e+03;	Best Local Similarity 40.0%; Pred. No. 2.3e+05;
	Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;	Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
Qy 1 VTQD 4	Qy 1 VTQDD 5	
Db 9 ITND 12	Db 1 MTND 5	
RESULT 20	RESULT 22	
ID 052640	Q83622	
AC 052640; PRELIMINARY;	ID Q83622	PRELIMINARY;
DT 01-JUN-1998 (TREMBLrel. 06, Created)	AC AC	PRT; 9 AA.
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)	DT DT	
DT 01-NOV-1998 (TREMBLrel. 06, Last annotation update)	DT DT	
DN NTNU (FRAGMENT).	DT DT	
GN NTNU.	DE DE HYPOTHETICAL PROTEIN (FRAGMENT).	
OS Pseudomonas sp.		

OS Murray valley encephalitis virus.
 OC ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 CC Flavivirus.
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 88118912.
 RA HAHN C.S., HAHN Y.S., RICE C.M., LEE E., DALGARNO L., STRAUSS E.G.,
 RA STRAUSS J.H.;
 RT "Conserved elements in the 3' untranslated region of flavivirus RNAs
 and potential cyclization sequences.";
 RR J. Mol. Biol. 198:33-41(1987).
 DR EMBL: M35172; AA666627; 1; -.
 KW Hypothetical protein; Repeat.
 FT NON_TER 1 1
 SQ SEQUENCE 9 AA: 1055 MW: 7EF99143 CRC32;

Query Match 37.1%; Score 13; DB 12; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.3e+05; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; PRT; 11 AA.

Qy 1 VTD 4
 Db 3 VSD 6

RESULT 23
 ID Q63056 PRELIMINARY; PRT; 10 AA.
 AC Q63056;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DE RAT ASIALOGLYCOPEPTIDE RECEPTOR (ASGP).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87026895.
 RA WATTS C.;
 RT "Isolation and expression of cDNA clones for a rat liver
 asialoglycoprotein receptor";
 RR Biosci. Rep. 6:522-534(1986);
 DR EMBL: M21739; AA0A0763.1; -.
 SQ SEQUENCE 10 AA: 1312 MW: 0908A0D9 CRC32;

Query Match 37.1%; Score 13; DB 11; Length 10;
 Best Local Similarity 50.0%; Pred. No. 6.e+03; Indels 0; Gaps 0;
 Matches 2; Conservative 0; Mismatches 0; PRT; 11 AA.

Qy 1 VTD 4
 Db 1 VTKD 4

RESULT 24
 ID Q16427 PRELIMINARY; PRT; 11 AA.
 AC Q16427;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE DYSTROPHIN PROTEIN (FRAGMENT).
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
 OC Fotheria; Primates; Catarrhini; Hominidae; Homo.
 [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 96163501.
 RA HOLDER E., MAEDA M., BIES R.D.;

RT "Expression and regulation of the dystrophin Purkinje promoter in
 human skeletal muscle, heart, and brain.";
 RL Hum. Genet. 97:132-239(1996).
 DR EMBL: S81419; AAD14362.1; -.
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1299 MW; AF0E38FF CRC32;

Query Match 37.1%; Score 13; DB 4; Length 11;
 Best Local Similarity 40.0%; Pred. No. 7e+03; Indels 0; Gaps 0;
 Matches 2; Conservative 2; Mismatches 1; PRT; 11 AA.

Qy 1 VTQDD 5
 Db 4 VSSDE 8

RESULT 25
 ID Q78119 PRELIMINARY; PRT; 11 AA.
 AC Q78119;
 DT 01-NOV-1998 (TREMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
 DE MAC CLASS II B LOCUS 1 (FRAGMENT)
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Actinopterygii;
 OC Neopterygii; Teleostei; Euteleostei; Acanthopterygii; Perciformes; Labroidei; Cichlidae; Oreoichromis.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 98151113.
 RA MALAGA-TRILLO E., MCANDREW B., ZALESKA-RUTCZYNKA Z.,
 RA SUDTMANN H., FIGUEROA F., KLEIN J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid fish
 class II B loci";
 RL Genetics 140:1527-1547(1999).
 DR EMBL: AF050017; AAC41356.1; -.
 KW MAC;
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1276 MW; AFCDDB5B5 CRC32;

Query Match 37.1%; Score 13; DB 7; Length 11;
 Best Local Similarity 60.0%; Pred. No. 7e+03; Indels 0; Gaps 0;
 Matches 3; Conservative 1; Mismatches 1; PRT; 11 AA.

Qy 1 VTQDD 5
 Db 7 VTRCD 11

RESULT 26
 ID Q36622 PRELIMINARY; PRT; 12 AA.
 AC Q36622;
 DT 01-NOV-1996 (TREMBLrel. 01, Created)
 DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
 DE CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE
 GN CHL-B.
 OS Picea abies (Norway spruce) (Picea excelsa).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae;
 OC Picea.
 RN SEQUENCE FROM N.A.
 RP TISSUE-COTYLEDONS.
 RC KARPINSKA B., KARPINSKI S., HILGREN J.E.;
 RA Curr. Genet. 0:0-0(0).
 RL

DR	EMBL; X98685; CAA67242.1; - .	KW	Chloroplast.	1	1
KW	Chloroplast.	FT	NON_TER	1	
FT	NON_TER 1	FT	NON_TER	12	12
FT	NON_TER 12	SEQUENCE	12 AA;	1445 MW;	75FC0606 CRC32;
SEQUENCE	12 AA;	1445 MW;	75FC0606 CRC32;		
Query Match	Score 13;	DB 8;	Length 12;		
Best Local Similarity	50.0%	Pred. No.	7.7e+03;		
Matches	2;	Mismatches	0;		
Indels	0;	Gaps	0;		
QY	4 DDLO 7	QY	4 DDLO 7	Score 13;	DB 8;
	:1 :			Pred. No.	7.7e+03;
Db	1 EDLK 4	Db	1 EDLK 4	Mismatches	0;
Indels	0;	Gaps	0;		
RESULT 27	Q36623	PRELIMINARY;	PRT;	12 AA.	
ID	Q36623;				
AC	036623;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)	AC	Q36623;	PRELIMINARY;	PRT;
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	12 AA.	
DT	01-NOV-1996 (TREMBLrel. 01, Last annotation update)	DT	01-NOV-1996 (TREMBLrel. 01, Last annotation update)		
DE	CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE REDUCTASE (FRAGMENT).	DE	CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE REDUCTASE (FRAGMENT).		
GN	CHLB.	GN	CHLB.		
OS	Pinus sylvestris (Scots pine).	OS	Pinus sylvestris (Scots pine).		
OG	Chloroplast.	OG	Chloroplast.		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.		
RN	[1]	RN	[1]		
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.		
RC	TISSUE=COLEOPTERANS;	RC	TISSUE=COLEOPTERANS;		
RA	KARPINSKA B., KARPINSKI S., HILGREN J.E.;	RA	KARPINSKA B., KARPINSKI S., HILGREN J.E.;		
RL	Curr. Genet. 0:0(0)	RL	Curr. Genet. 0:0(0)		
DR	EMBL; X98684; CAA67241.1; - .	DR	EMBL; X98684; CAA67241.1; - .		
KW	Chloroplast.	KW	Chloroplast.		
FT	NON_TER 1	FT	NON_TER 1		
FT	NON_TER 12	SEQUENCE	12 AA;	1475 MW;	7337C4ED CRC32;
SEQUENCE	12 AA;	1475 MW;	7337C4ED CRC32;		
Query Match	Score 13;	DB 8;	Length 12;		
Best Local Similarity	50.0%	Pred. No.	7.7e+03;		
Matches	2;	Mismatches	0;		
Indels	0;	Gaps	0;		
QY	4 DDLO 7	QY	4 DDLO 7	Score 13;	DB 8;
	:1 :			Pred. No.	7.7e+03;
Db	1 EDLK 4	Db	1 EDLK 4	Mismatches	0;
Indels	0;	Gaps	0;		
RESULT 28	Q36668	PRELIMINARY;	PRT;	12 AA.	
ID	Q36668				
AC	036668;				
DT	01-NOV-1996 (TREMBLrel. 01, Created)	AC	Q36668;	PRELIMINARY;	PRT;
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)	12 AA.	
DT	01-NOV-1996 (TREMBLrel. 01, Last annotation update)	DT	01-NOV-1996 (TREMBLrel. 01, Last annotation update)		
DE	CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE REDUCTASE (FRAGMENT).	DE	CHLOROPLAST SUBUNIT OF LIGHT INDEPENDENT PROTOCHLOROPHYLLIDE REDUCTASE (FRAGMENT).		
GN	CHLB.	GN	CHLB.		
OS	Pinus sylvestris (Scots pine).	OS	Pinus sylvestris (Scots pine).		
OG	Chloroplast.	OG	Chloroplast.		
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.	OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; euphyllophytes; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.		
RN	[1]	RN	[1]		
RP	SEQUENCE FROM N.A.	RP	SEQUENCE FROM N.A.		
RC	TISSUE=COLEOPTERANS;	RC	TISSUE=COLEOPTERANS;		
RA	KARPINSKA B., KARPINSKI S., HILGREN J.E.;	RA	KARPINSKA B., KARPINSKI S., HILGREN J.E.;		
RL	Curr. Genet. 0:0(0)	RL	Curr. Genet. 0:0(0)		
DR	EMBL; X98683; CAA67240.1; - .	DR	EMBL; X98683; CAA67240.1; - .		
EMBL; X98683; CAA67239.1; - .	EMBL; X98683; CAA67239.1; - .				

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DR EMBL; X98679; CAA67237.1; -.
KW Chloroplast.
FT NON-TER 1 1
FT NON-TER 12 12
FT MW; 75FC0606 CRC32;
SQ SEQUENCE 12 AA; 1445 MW;

Query Match 37.1%; Score 13; DB 8; Length 12;
Best Local Similarity 50.0%; Pred. No. 7.7e-03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 4 DDLQ 7
Db :||:
1 EDLK 4

Search completed: June 30, 2000, 16:18:45
Job time: 7896 sec

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